

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

OM nucleic - nucleic search, using sw model
Run on: June 19, 2003, 12:25:35 ; Search time 1554 Seconds
(without alignments)
15094.505 Million cell updates/sec

Title: US-09-966-881-13
Perfect score: 806
Sequence: 1 TGTCCTCTCCCTTCGATCACA.....TCCCTCTCTATGGATNG 806

Scoring table: IDENTITY_NUC
Gapext 10.0 , Gapext 1.0
Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : GenEtbl:
1: qb_ba: *
2: qb_htg: *
3: qb_in: *
4: qb_cm: *
5: qb_ov: *
6: qb_pat: *
7: qb_ph: *
8: qb_pl: *
9: qb_pr: *
10: qb_ro: *
11: qb_sts: *
12: qb_sy: *
13: qb_un: *
14: qb_vl: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_jmu: *
20: em_om: *
21: em_or: *
22: em_ov: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_vl: *
29: em_vn: *
30: em_htg_hum: *
31: em_htg_inv: *
32: em_htg_other: *
33: em_htg_mus: *
34: em_htg_pln: *
35: em_htg_rnd: *
36: em_htg_mam: *
37: em_htg_vrt: *
38: em_sy: *
39: em_htgo_hum: *
40: em_htgo_mus: *
41: em_htgo_other: *

Result No.	Score	Query Match	% Length	DB	ID	Description
1	778	95.5	805	6	A70152	A70152 Sequence 13
2	612.4	76.0	1788	8	AF206320	AF206320 Musa acum
3	591.8	73.4	748	6	A83011	A83011 Sequence 18
4	591.2	73.3	745	6	A83004	A83004 Sequence 11
5	588.8	73.1	793	6	A83001	A83001 Sequence 8
6	588.8	73.1	793	8	MAZ9965	Z9965 Musa acum
7	572.2	71.9	727	6	A83014	A83014 Sequence 21
8	543.8	67.5	727	6	A70155	A70155 Sequence 16
9	536	66.5	724	6	A70157	A70157 Sequence 18
10	510.8	63.4	704	8	A83000	A83000 Sequence 7
11	496.8	61.6	705	6	A83012	A83012 Sequence 19
12	174.4	21.6	127202	2	OSJN0272	AL731627 Oryza sat
13	169.4	21.0	1633	8	AY085026	AY085026 Arabidops
14	152	18.9	90142	8	ATAC016827	AC016827 Arabidops
15	151	18.7	823	6	A83003	A83003 Sequence 10
16	150	18.6	1403	8	FXU63550	U63550 Fragaria x
17	148	18.4	1523	8	AY086099	AY086099 Arabidops
18	144.8	18.0	1495	8	AF206319	AF206319 Musa acum
19	144.4	17.9	749	6	AB2999	AB2999 Sequence 6
20	143.2	17.8	1462	8	MAPEL	X92943 Macuminate
21	142.8	17.7	842	6	A70156	A70156 Sequence 17
22	141.4	17.5	703	6	A83002	A83002 Sequence 9
23	141	17.5	1525	8	AY050404	AY050404 Arabidops
24	141	17.5	1556	8	AY050795	AY050795 Arabidops
25	134.6	16.7	687	8	A70153	A70153 Sequence 14
26	134.6	16.7	687	8	MAZ9977	Z9977 Musa acum
27	133.2	16.5	5368	8	AF339024	AF339024 Fragaria
28	131.6	16.3	772	8	MAZ9970	MAZ9970 Musa acum
29	131.6	16.3	758	6	A83005	A83005 Sequence 12
30	131	16.3	1431	8	AY05197	AY05197 Arabidops
31	130.4	16.2	794	6	A83006	A83006 Sequence 13
32	129.2	16.0	728	6	A83013	A83013 Sequence 20
33	128.8	16.0	131	6	A83010	A83010 Sequence 17
34	128.4	15.9	745	6	AB3008	AB3008 Sequence 15
35	127.2	15.8	1782	8	AY087724	AY087724 Arabidops
36	127	15.8	1065	8	AY06033	AY06033 Arabidops
37	127	15.8	1459	8	AY065034	AY065034 Arabidops
38	127	15.8	1788	8	AY054200	AY054200 Arabidops
39	126.2	15.7	731	6	A83009	A83009 Sequence 16
40	124	15.4	1440	6	AX05936	AX05936 Sequence 16
41	124	15.4	1440	8	ZEPCKX	Y0541_2_elegans m
42	123.6	15.3	4143	8	AF339025	AF339025 Fragaria
43	122.6	15.2	10079	8	TG11	AC002376 Sequence
44	122	15.1	6172	8	AB017061	AB017061 Arabidops
45	122	15.1	81662	8	AB008265	AB008265 Arabidops

ALIGNMENTS

RESULT 1
A70152
LOCUS A70152 Sequence 13 from Patent WO981228.
DEFINITION Sequence 13 from Patent WO981228.
ACCESSION A70152
VERSION A70152.1 GI:4774567
KEYWORDS
SOURCE
ORGANISM unidentified.
unclassified.
REFERENCE 1 (bases 1 to 806)
AUTHORS Seymour, G.B., Bird, C.R. and Medina-Suarez, R.D.
TITLE GENETIC CONTROL OF FRUIT RIPENING
JOURNAL PATENT: WO 981228-A 13 19-MAR-1998.
SEYMON GRAHAM BARRON (GB)

FEATURES		ACCESSION	AP206320
SOURCE	Location/Qualifiers	VERSION	AP206320.1
BASE COUNT	1. . 806	GI	6606533
ORIGIN	/organism="unidentified" /db_xref="taxon:2644" /clone="U-U68"	SOURCE	Musa acuminata
Query Match	96.5%; Score 778; DB 6; Length 806;	REFERENCE	1 (bases 1 to 1788)
Best Local Similarity	100.0%; Pred. No. 3-8e-193;	AUTHORS	Ong, C.K., Pua, E.C. and Liu, P.
Matches	806; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	TITLE	Molecular cloning and characterization of pectate lyase in banana
QY	1 TGTCTCTCTCTGATCAATCTTGTGCTGTGGAAGAGTGAAGGTAGACCGAGGGG 60	JOURNAL	Unpublished
Db	1 TGTCTCTCTGATCAATCTTGTGCTGTGGAAGAGTGAAGGTAGACCGAGGGG 60	REFERENCE	2 (bases 1 to 1788)
QY	61 GCAATGACGGGGGTTAGATGGATTCTCTCTGCTCTCTCTGCTCTGGCTCC 120	AUTHORS	Ong, C.K., Pua, E.C. and Liu, P.
Db	61 GCAATGACGGGGGTTAGATGGATTCTCTCTGCTCTGGCTCC 120	TITLE	Submitted (18-NOV-1999), Department of Biological Sciences, National
QY	121 CTGGTTTGAACGGGGTGGGGGATGGAGACGGAGCTGGCTCTGCTCTGGCTCC 120	JOURNAL	University of Singapore, 10 Kent Ridge Crescent, Singapore 119260
Db	121 CTGGTTTGAACGGGGTGGGGGATGGAGACGGAGCTGGCTCTGCTCTGGCTCC 120	FEATURES	Location/Qualifiers
QY	181 GGCAGAGCATCGGGGAGGGACTTGGAGAGGAGGCTCGGGGAGGGGGGG 240	source	1. . 1788
Db	181 GGCAGAGCATCGGGGAGGGACTTGGAGAGGAGGCTCGGGGAGGGGGGG 240	/organism="Musa acuminata" /cultivar="Williams" /db_xref="taxon:4641"	/organism="Musa acuminata" /cultivar="Williams" /db_xref="taxon:4641"
QY	241 TCCCTGGAGAGAGGGCTTAACCGGGCAGCAGAGGGGGGGGGGGGGGGGG 300	gene	1. . 1788
Db	241 TCCCTGGAGAGAGGGCTTAACCGGGCAGCAGAGGGGGGGGGGGGGGGGG 300	CDS	/gene="Pl2" /codon_start=1
QY	301 GTGCTCTGAGGGCTGATGACCATAATCAACAGCAGCAGCAGCAGCAGCAG 300	/product="pectate lyase 2" /protein_id="AAF9195.1" /db_xref="GI:6606534"	/product="pectate lyase 2" /protein_id="AAF9195.1" /db_xref="GI:6606534"
Db	301 GTTGGTCCACGGCTCTGATGACCTTAATCAACAGCAGCAGCAGCAGCAG 360	REFERENCE	/translation="MTAQLRWPULLLGLFLVLRSGWGSNSSGNSRGGASR RSUREASINATSDASADAEVTRAVTAEDVPEEVASTVLTILNTRSSRGVLS GSNPIDOCWRCDPWHNRKKIADGGFFRRAIGGDGEVLUVTSGDDEPVNP GTIRYAVQDVPWITHEMDEITKELMNSFKTIDGYNVHNTAGCTIQTY ~NVIHGHLHDKPRTGNAWHRMFSHITWADGDAVSJFOSSHITWADHSLSCAD GLYDVKMSTATTVSNNFTHNEMVLIGHTSYAROSIMQVTAIFNHFGEIQLRNP RCHHGTYFIVVNUDYTHWNYATGSANNTINSQRNLTAPTPFAKENTKRYTDOST WKNWNRREGDILLNGAFTTPSGAGASASAYARASSFGKPKSSLVLTSDAGVLSCQ GTRC
QY	361 CTGCTGTGGTTCAGCAACCGATCGAGACTCTGGGGTGGACCCCTGATGGCA 420	BASE COUNT	419 a
Db	361 CTGCTGTGGTTCAGCAACCGATCGAGACTCTGGGGTGGACCCCTGATGGCA 420	ORIGIN	473 c
QY	421 GTCAACAGAAAAGCTCCGTACTGCGCATGGCTTGGACCAACCCNATANTGTC 480	BASE COUNT	419 a
Db	421 GTCAACAGAAAAGCTCCGTACTGCGCATGGCTTGGACCAACCCNATANTGTC 480	ORIGIN	473 c
QY	481 CGCGACGGGAAATTGTGTTGTCAGACAGACTCCGGGACNATGCCCGTGATCC 540	Query Match	76.0%; Score 612.4; DB 8; Length 1788;
Db	481 CGCGACGGGAAATTGTGTTGTCAGACAGACTCCGGGACNATGCCCGTGATCC 540	Best Local Similarity	88.6%; Pred. No. 1e-149
QY	541 GCCCGGAAACTTANATACCCGTCNTCAANGAGTGGCCCTCTGGATCCCTT 600	Matches	716; Conservative 0; Mismatches 82; Indels 10; Gaps 6;
Db	541 GCCCGGAAACTTANATACCCGTCNTCAANGAGTGGCCCTCTGGATCCCTT 600	QY	1 TGTCTCTCTGATCACATCTTGTGCTGTGGAAGCTGTGAGACGGGGGG 60
QY	601 AAACNCNAATGGAAATCTNCNTCAANGAGAAGCTNTATGACGAGCTTAACNACNT 660	Db	15 TGTCTCTCTGATCACATCTTGTGCTGTGGAAGCTGTGAGACGGGGGG 74
Db	601 AAACNCNAATGGAAATCTNCNTCAANGAGAAGCTNTATGACGAGCTTAACNACNT 660	QY	61 GCAATGACGGGGTTTAAGATGGATGGATGGATGGATGGATGGATGGATGG 120
QY	661 CGATGACGACGCTGTCACATTGCAATGGCCTGCMTCACCAANCAATTG 720	Db	61 GCAATGACGGGGTTTAAGATGGATGGATGGATGGATGGATGGATGG 120
Db	661 CGATGACGACGCTGTCACATTGCAATGGCCTGCMTCACCAANCAATTG 720	QY	75 GCAATGACGGGGTTTAAGATGGATGGATGGATGGATGGATGGATGG 134
QY	721 TCCCAACACTCTCCCTGCTCCATGGACACCCGGGAATTCCTG 780	Db	121 CTGGTTTGACGGGGTGGGGGGATGGAGAGGCTGGAGAGGAGGCTGGAGGAAT 180
Db	721 TCCCAACACTCTCCCTGCTCCATGGACACCCGGGAATTCCTG 780	QY	135 CTGGTTTGACGGGGTGGGGGGATGGAGAGGCTGGAGAGGAGGCTGGAGGAAT 194
QY	781 CCCCNCTCCCTCTCTGATGGATGG 806	Db	181 GGCAGACATCGGCAGGGCTGGAGAGGCTGGAGAGGAGGCTGGAGGAAT 240
Db	781 CCCCNCTCCCTCTGATGGATGG 806	QY	195 GGCAGACATCGGCAGGGCTGGAGAGGAGGCTGGAGAGGAGGCTGGAGGAAT 254
RESULT 2	AF206320	QY	241 TCCCTGGAGAGGGCTGGAGAGGCTGGAGAGGAGGCTGGAGAGGAGGCTGGAGGAAT 300
LOCUS	AF206320	Db	255 TCCCTGGAGAGGGCTGGAGAGGAGGCTGGAGAGGAGGCTGGAGAGGAGG 314
DEFINITION	Musa acuminata pectate lyase 2 (PL2) mRNA, complete cds.	QY	301 GTCGCGTGCAGGGCTGGAGAGGAGGCTGGAGAGGAGGCTGGAGAGGAGGCTGGAGGAAT 360
		Db	315 GTCGCGTGCAGGGCTGGAGAGGAGGCTGGAGAGGAGGCTGGAGAGGAGGCTGGAGGAAT 374
		QY	361 GTCGCGTGCAGGGCTGGAGAGGAGGCTGGAGAGGAGGCTGGAGAGGAGGCTGGAGGAAT 420
		Db	375 GTCGCGTGCAGGGCTGGAGAGGAGGCTGGAGAGGAGGCTGGAGAGGAGGCTGGAGGAAT 434

QY	421 GTCACACAGAAAAAGCTCGCTGACTGGCATTTGGACGCAACGCNATANGTGC	480	QY	241 TCTTGGAGAGGGCTGTAACCGGGCAGGAGAACGCCAGTCAGACCCGAGG	300
Db	435 GTCACACAGAAAAGCTCGCTGACTGGCATTTGGACGCAACGCNATANGTGC	494	Db	256 TCTTGGAGAGGGCTGACCGCAGAACGCCAGTCAGACCCGAGG	315
QY	481 CGCGACGGGAATTTGTCGTTGAGAGACTCCGGACNATGATCCCGTGAATTC	540	QY	301 GTCGTCGACGCTTCGATGACCTATTCAGACGACGGCAGTCAGATCTGGT	360
Db	495 CGCGACGGG-AGTTGTCAGTGTGACAGACTCCGGACGATGATCCCGTGAATTC	552	Db	316 GTGCTTGACGGTCTGACGACCATATCACAGACGGCAGTCAGATCTGGT	375
QY	541 GCGGGGACACTTANATACCCGTCWCCANGAAGTGGCCCTGTTGGATCCCTT	600	QY	361 CGTCGTCGCGGTTGAGGACCCGATGACGACTGCGGCGCTGACCCGTGATGGC	420
Db	553 GCGGGGACACTTATACCCGTCWCCANGAAGTGGCCCTGTTGGATCCCTT	608	Db	376 CGTCGTCGCGGTTGAGGACCCGATGACGACTGCGGCGCTGACCCGTGATGGC	435
QY	601 AACNCNAAANTGGAATCTCNCNCNANGAAGAACONTATGACAGCTTAAACNAT	660	QY	421 GTCACACAGAAAAGCTCGCTGACTGGCATTTGGACGCAACGCNATANGTGC	480
Db	609 AACACCGATGGAGATCACCGCT-AGAGGAACTTATGACAGCTTAAACGAT	667	Db	436 GTCACACAGAAAAGCTCGCTGACTGGCATTTGGACGCAACGCNATANGTGC	495
QY	661 CGATGGACNCNGTGTCCACATGGCCATGCCCCTGTCACACANCAATTTCN	720	QY	481 CGCGACGGGAATTGTCGTCGTTGACAGACCTGGGACNATGATCCCGTGAATCTC	540
Db	668 CGATGGACGGGGTCAACGTCACATGGCCATGCGCATCACATCC-AGTACA	726	Db	496 CGCGACGGGANITGTAGTGTGAGAGACTCCGGGACNATGATCCCGTGAATCTC	555
QY	721 TCCCCACNTCTCCNTNCNTCCNC- TCCCCATGCAACCCNCGGGAATTCCN	778	QY	541 GCGGGGACACTTANATACCCGTCWCCANGAAGTGGCCCTCTGGATCCCTT	600
Db	727 TCACCAAGTCACTATCCACGCTCACCACACTGCAAGCCACCGGAATGCCA	786	Db	556 CGCGGGACACTTANATACCCGTCWCCANGAATGTCACCCCTGTCACACATTC	610
QY	779 GTCACACAGTCCTCTCTATGGATG 806		QY	601 AACNCNAAANTGGAATCTCNCNCNANGAAGAACONTATGACAGCTTAAACNAT	660
Db	787 TGGTCCCCAGCTCCCTCACTATGG 814		Db	611 AACACCGACNTGAAACATCCACGCTCACCACACTGCAAGCCACGCTTAAACAT	669
RESULT 3					
A83011	A83011	748 bp	DNA	linear	PAT 21-JAN-2000
LCCUS	DEFINITION	Sequence 18 from Patent WO9853085.			
ACCESSION	VERSION	A83011.1			
KEYWORDS	SOURCE	unidentified			
ORGANISM	unclassified				
REFERENCE	1 (bases 1 to 748)				
AUTHORS	Seymour, G.B. and Bird, C.R.				
TITLE	GENETIC CONTROL OF FRUIT RIPENING				
JOURNAL	PATENT: WO 9853085-A 18 26-NOV-1998;				
FEATURES	SOURCE	SEYMOUR GRAHAM BARRON (GB); ZENECA LTD (GB)			
	1. .748				
	/organism="unidentified"				
	/db_xref="taxon:32644"				
	/clone="U-113"				
BASE COUNT	154	a 211 c 206 g 163 t 14 others			
ORIGIN					
Query Match	73.4%	Score 591.8; DB 6; Length 748;			
Best Local Similarity	91.7%	Pred. No. 2.5e-144; Indels 8; Gaps 4;			
Matches	664;	Conservative 0; Mismatches 52;			
QY	1 TGTTCCTCTCTGATCACATCTTGTCTCGGAAACCTGAGAGCTGAGAGGGCG	60	QY	1 TGTTCCTCTCTGATCACATCTTGTCTCGGAAACCTGAGAGCTGAGAGGGCG	60
Db	16 TGTTCCTCTCTGATCACATCTTGTCTCGGAAACCTGAGAGCTGAGAGGGCG	75	Db	241 TCTTGGAGAGGGCTGTAACCGGGCAGGAGAACGCCAGTCAGACCCGAGG	300
QY	61 GCAATGAGGGCGGTTAAGATGATCTCTCTCTGCTCTCTCTGCTCTCTCTG	120	QY	256 TCTTGGAGAGGGCTGACCGCAGAACGCCAGTCAGACCCGAGG	315
Db	76 GCAATGAGGGCGGTTAAGATGATCTCTCTCTGCTCTCTCTGCTCTCTCTG	135	Db	301 GTCGTCGACGCTTCGATGACCTATTCAGACGACGGCAGTCAGATCTGGT	360
QY	121 CGGGTCTGAGCGGGCTCGGGGTGTTGAGAGGAGTCGGGAGGAGGCTCTGGCTGAGGAT	180	Db	316 GTGCTTGACGGTCTGACGACCATATCACAGACGGCAGTCAGATCTGGT	375
Db	136 CGGGTCTGAGCGGGCTCGGGGTGTTGAGAGGAGTCGGGAGGAGGCTCTGGCTGAGGAT	195	QY	361 CGTCGTCGCGGTTGAGGACCTGTCCTCCCTGCTCTCTCTGCGCTCTG	420
QY	181 CGCGGACATCGGGAGGAGCTGAGAGGAGTCGGGAGGAGGCTCTGGCTGAGGAT	240	Db	376 CGTCGTCGCGGTTGAGGATGATCTCTCTCTGCTCTCTCTGCGCTCTG	435
Db	196 CGCGGACCATCGGGAGGAGCTGAGAGGAGGCTCCGGACAGCGACCGCG	255	QY	421 TCTTGGAGAGGGCTGTAACCGGGCAGGAGAACGCCAGTCAGACCCGAGG	300
QY	121 CGGGTCTGAGCGGGCTCGGGGTGTTGAGAGGAGTCGGGAGGAGGCTCTGGCTGAGGAT	180	QY	436 GTCACACAGAAAAGCTCGCTGACTGGCATTTGGACGCAACGCNATANGTGC	495

RESULT 8

AT0155 LOCUS 727 bp DNA linear PAT 07-MAY-1999

DEFINITION Sequence 16 from Patent WO9811228.

ACCESSION A70155

VERSION A70155.1

KEYWORDS G1:4774570

SOURCE unidentified.

ORGANISM unclassified.

REFERENCE 1 (bases 1 to 727)

AUTHORS Seymour, G. B., Bird, C. R. and Medina-Suarez, R. D.

TITLE GENETIC CONTROL OF FRUIT RIPENING

JOURNAL PATENT: WO 9811228-A 16 19-MAR-1998;

SEYMOUR GRAHAM BARRON (GB)

FEATURES source

1. . 727

/organism="unidentified"

/db_xref="taxon:32644"

BASE COUNT 145 a 205 c 196 g 159 t 22 others

Query Match 67.5%; Score 543 8; DB 6; Length 727;

Best Local Similarity 86.6%; Pred. No. 9.8e-132; Mismatches 91; Indels 6; Gaps 4;

Matches 62B; Conservative 0; Mismatches 91; Indels 6; Gaps 4;

QY 2 GTTCCTCTCTCGATCACATCTTGTCTGGAAACCTGAGAGGTGAGACGAGGGGG 61

Db 8 GTTCCTCTCTCGATCACATCTTGTCTGGAAACCTGAGAGGTGAGACGAGGGGG 67

QY 62 CAATACGGCGGGGTTAACATGGATCTCCCTCTGCTCTCTGGCTCC 121

Db 68 CAATACGGCGGGGTTAACATGGATCTCCCTCTGCTCTCTGGCTCC 127

QY 122 TGGTTTGTGAACGGGAGTCGGGGTGAACGGAGGGTCTCTGGCTCGAGGAATG 181

Db 128 TGGTTTGTGAACGGGAGTCGGGGTGAACGGAGGGTCTCTGGCTCGAGGAATG 187

QY 182 GGGGACATGGGAGGACTGTGAGAGAGGCTCGGAGCGACGGACACGGCGATGCT 241

Db 188 GGGGACATGGGAGGACTGTGAGAGAGGCTCGGAGCGACGGACACGGCGATGCT 247

QY 242 CCTGGAAAGAGGGCTGTACCGGAGGCTGTACCGGAGGCTGTACCGGAGGAGG 301

Db 248 CCTTGAAAGAGGGCTGTACCGGAGGCTGTACCGGAGGCTGTACCGGAGGAGG 307

QY 302 TTGCTCTGAGGTCTGTATGACCAATAATCACAGCACGCCTCGAGATGTCTGGTATC 361

Db 308 TTGCTCTGAGGTCTGTACCGGAGGCTGTACCGGAGGCTGTACCGGAGGAGG 367

QY 362 TTGCTCTGAGGTCTGTACCGGAGGCTGTACCGGAGGCTGTACCGGAGGAGG 421

Db 368 TTGCTCTGAGGTCTGTACCGGAGGCTGTACCGGAGGCTGTACCGGAGGAGG 427

QY 422 TTGCTCTGAGGTCTGTACCGGAGGCTGTACCGGAGGCTGTACCGGAGGAGG 480

Db 428 TTGCTCTGAGGTCTGTACCGGAGGCTGTACCGGAGGCTGTACCGGAGGAGG 487

QY 481 CGCGAGGGGAATTTGTCGTGAGACACTCGGGGAGNATGATCCCGTGAATCTC 540

Db 488 CGCCACNGGAGNTGTCGTGAGACACTCGGGGAGGATGAT-CCGTGATCTC 546

RESULT 9

A70157 LOCUS 724 bp DNA linear PAT 07-MAY-1999

DEFINITION Sequence 18 from Patent WO9811228.

ACCESSION A70157

VERSION A70157.1

KEYWORDS G1:4774572

SOURCE unidentified.

ORGANISM unclassified.

REFERENCE 1 (bases 1 to 724)

AUTHORS Seymour, G. B., Bird, C. R. and Medina-Suarez, R. D.

TITLE GENETIC CONTROL OF FRUIT RIPENING

JOURNAL PATENT: WO 9811228-A 18 19-MAR-1998;

SEYMOUR GRAHAM BARRON (GB)

FEATURES source

1. . 724

/organism="unidentified"

/db_xref="taxon:32644"

BASE COUNT 143 a 201 c 197 g 155 t 28 others

Query Match 66.5%; Score 536; DB 6; Length 724;

Best Local Similarity 89.7%; Pred. No. 1.1e-129; Mismatches 62; Indels 9; Gaps 5;

Matches 617; Conservative 0; Mismatches 62; Indels 9; Gaps 5;

QY 6 TCTCCCTGATCACATCTTGTCTGGCTCTGGAAACCTGAGAGGTGAGACGGGGCAAT 65

Db 9 TCTCCCTGATCACATCTTGTCTGGCTCTGGAAACCTGAGAGGTGAGACGGGGCAAT 68

QY 126 TTGACGGAGGTCTGGGGTGAACGGAGGGCTCTGGCTCGAGGAATGGCG 185

Db 129 TTGACGGAGGTCTGGGGTGAACGGAGGGCTCTGGCTCGAGGAATGGCG 188

QY 186 AGCATGGGAGGACTGTGAGAGAGGCTCGGAGGCTCGAGGAGGCTCGAGGATGCT 245

Db 189 AGCATGGGAGGACTGTGAGAGAGGCTCGGAGGCTCGAGGAGGCTCGAGGATGCT 248

QY 246 GGAAGAGAGGCTGTACCGGGAGGAGGAGGCTCGAGGAGGCTCGAGGATGCT 305

Db 249 GGAAGAGAGGCTGTACCGGGAGGAGGAGGCTCGAGGAGGCTCGAGGATGCT 308

QY 306 TTGCGGGCTGTAGACCAATAACAGCACGGCTCGAGATCTCTGGTATCTC 365

Db 309 TTGCGGGCTGTACCGGGAGGAGGAGGCTCGAGGAGGCTCGAGGATGCT 368

QY 366 TTGCGGGCTGTACCGGGAGGAGGAGGCTCGAGGAGGCTCGAGGAGGCTCGAGGATGCT 425

Db 369 TTGCGGGCTGTACCGGGAGGAGGAGGCTCGAGGAGGCTCGAGGAGGCTCGAGGATGCT 428

QY	426 CAGAAAAAGCTGCTGACTGGCCATGGCCTTGGACGCAACGCNATANGTGGCCCGCA 485	Db	365 GGTTTCAAGCAACCCGATGACINACTGCTGGGGTGGACCCGATGCTACAGA 424				
Db	429 CAGAAAAAGCTGCTGACTGGCCATGGCCTTGGACGCAACCCGATANGTGGCCCGA 488	QY	429 AAAAAGCTGCTGACTGGCCATGGCCTTGGACGCAACCCGATANGTGGCCCGA 488				
QY	486 CGGGAAATTGTCGTCGTTGACAGACTCGGGGACNATGATCCCGTGAATCTCGCCCG 545	Db	425 AAAAAGCTGCTGACTGGCCATGGCCTTGGACGCAACGCATANGTGGCCCGA 484				
Db	489 CGGG -ANTTGTGTTGCTGACAGACTCGGGGACGATGATCCCGTGAATCTCGCCCG 547	QY	489 GGATTGGTGGTGGACAGACTCCGGGACNATGATGATCCCGTGAATCTCGCCCGA 548				
QY	546 CGAACACTTANATACCCGCTCNCCTTAAACN 605	Db	485 GG -ANTTGTACATGTCGACAGACTCCGGGACGATGATCCCGTGAATCTCGCCCGA 542				
Db	548 GGACACTTANAT -NCCGCTCNCCTTAAAC 603	QY	549 ACATTAAATAC -CCCGCTCNCCTTAAAC 607				
QY	606 CNAANTGAAATCTCNCCTNANGAAGAACACTTATGACAGC -TTAACNATCGA 663	Db	543 ACACTTANATACCCGCTCNCCTAANGAAT -GCCCTCTGGATCNCCTTAAACCC 600				
Db	604 C - ACNTGAGANATCCCNAGAACACTCTTAAACATCGAT 661	QY	608 AATGGAAACTCTCNCCTNANGAAGAACACTTATGACAGC 667				
QY	664 TGGACNCNGTGTCTCGTCCACATTGGC 691	Db	601 ACNTGAAATCTCNCCTNANGAAGAACACTTATGACAGC 660				
Db	662 NGGACCCNGTTTCACTTCCNCATTNGC 689	QY	668 CNGTGTCTCCACATTGGCAATGGCGCT 702				
RESULT 10							
LOCUS	A83000	ACCESSION	A83000				
DEFINITION	Sequence 7 from Patent WO9853085.	VERSION	GI:6732480				
KEYWORDS	unidentified	ORGANISM	unclassified				
REFERENCE	1 (bases 1 to 704)	AUTHORS	Seymour, G. B. and Bird, C. R.				
AUTHORS	Seymour, G. B. and Bird, C. R.	TITLE	GENETIC CONTROL OF FRUIT RIPENING				
JOURNAL	Patent: WO 9853085-A 7 26-NOV-1998;	FEATURES	SEYMON GRAHAM BARRON (GB); ZENECA LTD (GB)				
FEATURES	Location/Qualifiers	source	1. -704				
FEATURES	/organism="unidentified"	source	/db_xref="taxon:32644"				
BASE COUNT	146 a 190 c 191 g 149 t 28 others	ORIGIN	;				
BASE COUNT	146 a 190 c 191 g 149 t 28 others	ORIGIN	;				
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.	4	4e-123;	Mismatches	603;
Matches	0;	Mismatches	86;	Indels	6;	Gaps	5;
Query Match	63.4%	Score	510.8;	DB	6;	Length	704;
Best Local Similarity	86.8%	Pred.	No.				

/db_xref="GI:6728998",
 /translation="MSGESESYRKROPMDMGYHKRSAGLNPCKHSGFSISSLRPMAPG
 /TYPE=PKSSLRROVHAPVRLINSGRDRSTPQSGSNVLFPLTRNNMDMMKRNALDSSL

Query Match 18.9%; Score 152; DB 8; Length 90142;
 Best Local Similarity 63.5%; Pred. No. 9_9e-29;
 Matches 277; Conservative 0; Mismatches 152; Indels 7; Gaps 4;

Qy 317 TGATGACCTAACTAACGACGACGCTCCAGATCTCTGGTATCTGCGCGTGGTGTAG 376
 Db 53474 TCGAGGAGATCGAACAGCACAGAGCGGAGAAGATAGGTACTCTCTCGGCCACCG 53415

Qy 437 TCGTGAATGCGGATGCGTGGACCCAGATGGCATGTCACAGAAAAAGC 436
 Db 53414 GCACCCCATCGACGATGCTGGCGTCCGCGCAATAGCGCTCGCAAGCGT 53355

Qy 497 TGCGTTGAGACAGACTCGGGGACNATATCCCGTGAATCCCGTCTGGCGGGACACTTAN 556
 Db 53295 TACGTCGTAACCGACCTGGAGACGACCAT-CCGTTATCCATACCGGGACACCTCG 53237

Qy 557 ATACCCCTCTTCAAANGAAGTGGCCCTCTGGACGCCACGGCCGAC-GTCGTTTC 53296
 Db 53236 TCACGCCGATTC---AAGACGACACTCGGATCATCTTCGAAGGACATGGTA 53181

Qy 617 TCTCTCTGANGAAGAACNTATGACAGACAGCTTAAACNACNATGATGGACNNGCTC 676
 Db 53180 TAAC-CTTGAGGAAGAGCTGATCATGACAGCTTCAAACCATCGATGGTCTGGTTC 53122

Qy 677 CTGTCCTCATGCCAATGGCGCCTGCTCACCCANCCATTCTCTCCCAACNTCTCTT 736
 Db .53121 AATGTCACATGCCATTGGAGCTGTCACGATTCATACCTTACGACATATTGTC 53062

Qy 737 CCWNGCTCCNCTC 752
 Db 53061 CATGGGATTCATGTC 53046

RESULT 15

A83003
 LOCUS A83003
 DEFINITION Sequence 10 from Patent WO9853085.
 ACCESSION A83003
 VERSION A83003.1
 KEYWORDS SOURCE
 ORGANISM unidentified.
 unclassified.
 1 (bases 1 to 823)
 REFERENCE
 AUTHORS Seymour, G.B. and Bird, C.R.
 TITLE JOURNAL Patent: WO 9853085-A 10 26-NOV-1998;
 FEATURES
 source
 1. .823
 /organism="unidentified"
 /db_xref="taxon:32644",
 /clone="U-51",

BASE COUNT 168 a 222 g 150 t 17 others
 ORIGIN 266 c

Query Match 18.7%; Score 151; DB 6; Length 823;
 Best Local Similarity 63.7%; Pred. No. 9_9e-29;
 Matches 272; Conservative 0; Mismatches 149; Indels 6; Gaps 4;

Qy 327 AACCAACGACACGCTCCAGATCTCTGGTATCTGCGCGTGGTCAAGGAAACCGAT 386
 Db 137 AACCTGAGCTGCTGCCGGCGGAGCTGGCTACTGTCATGGCATGGCACCGGCAATCCGAT 196

Qy 387 CGACGACTGCTGGGGTGGACCTGATGGCATGTCACAGAAAAAGCTGCTGACTG 446

Search completed: June 19, 2003, 13:31:46
 Job time: 1557 secs

Db 197 CGACGACTGCTGGGGTGGACATCTGACTGGGCCACACCGGAGCGCTGGGGACTG 256
 Qy 447 CGGATGCTTGGACGCAACGCGATANGTGGCGACGGGGATTGTCGTTG 506
 Db 257 CGCCATGGTGGGAGAACCGATGGGGGGGACGCG-ACATATAGTGCTGA 315
 Qy 507 CAGACTCGGGGACNATATCCCGTGAATCCCGTCTGGCGGGAAACNTATGACATGGCGTC 566
 Db 316 CCGCAGTGGCGAGACGA-CCCCGTATCCGAGCGGGGAGCTCCGGTACGGCGT 374
 Qy 567 NTCCAAAGTGTGCCCCCTGGATGCCATGGAGGCCACGGGAATTG 496
 Db 375 ATCCAGGAGGAGCCGCTG--GGATCATCTTCAGCGCGACATGGTCATC-CAGTGA 430
 Qy 627 NGGAGAAACTCTNTATGACAGCTTAAACNACNATGATGGACNNGTCTCTGGCACA 686
 Db 431 AGAGAGCTCATGACTCCACACGACATGGCCACGAGCTGACCTGGTA 490
 Qy 687 TTGCCAATGGCGCTGCNTCACGCCAACNTCTCTCCNNGCTC 746
 Db 491 TCTCCGGGGCCCTGCATCACCAACCCAGTACGTCCACCAACATCATCCAGGGCTC 550
 Qy 747 CNCCTCC 753
 Db 551 CACATCC 557



GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2003, 11:17:55 ; (Search time 181 Seconds)

Sequence: 1 TGTCTCTCCTTCGGATCACA.....TCCCCTCTCTCTATGGATNG 806 (without alignments)

1028.236 Million cell updates/sec

Title: US-09-966-881-13
Perfect score: 806
Sequence: 1 TGTCTCTCCTTCGGATCACA.....TCCCCTCTCTCTATGGATNG 806

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters:

4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_101002:*

1: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1980.DAT:*

2: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1981.DAT:*

3: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1982.DAT:*

4: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1983.DAT:*

5: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1984.DAT:*

6: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1985.DAT:*

7: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1986.DAT:*

8: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1987.DAT:*

9: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1988.DAT:*

10: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1989.DAT:*

11: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1990.DAT:*

12: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1991.DAT:*

13: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1992.DAT:*

14: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1993.DAT:*

15: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1994.DAT:*

16: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1995.DAT:*

17: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1996.DAT:*

18: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1997.DAT:*

19: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1998.DAT:*

20: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1999.DAT:*

21: /SIDS2/gcdata/geneseq/geneseq-emb1/NA2000.DAT:*

22: /SIDS2/gcdata/geneseq/geneseq-emb1/NA2001.DAT:*

23: /SIDS2/gcdata/geneseq/geneseq-emb1/NA2002.DAT:*

ALIGNMENTS

RESULT 1

AVV28655
ID AVV28655 standard; cDNA; 806 BP.

XX AC AVV28655;

XX DT 29-JUL-1998 (first entry)

XX DE Ripening banana pulp cDNA clone D-U68 SEQ ID NO:13.

XX KW Banana; ripening; pulp; *Musa acuminata* cv. Grand Nain; fruit; genetic control; tissue senescence; ss.

XX OS Musa acuminata.

XX PN W09811228-A2.

XX PD 19-MAR-1998.

XX PF 08-SEP-1997; 97WO-GB02424.

XX PR 25-APR-1997; 97GB-0008366; 96GB-0018862.

XX PA (ZENE) ZENECA LTD.

XX PI Bird CR, Medina-Suarez RDJ, Seymour GB;

XX DR WPI; 1998-207389/18.

XX PT Modulation of ripening or tissue senescence in bananas - comprises use of DNA isolated from ripening banana pulp to produce genetically

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	778	96.5	806	19 AAV28655	Ripening banana pu
2	591.8	73.4	748	20 AAV69457	Banana fruit ripe
3	591.2	73.3	745	20 AAV69450	Banana fruit ripe
4	588.8	73.1	793	20 AAV69447	Banana fruit ripe
5	572.2	71.0	727	20 AAV69460	Banana fruit ripe
6	543.8	67.5	727	19 AAV28658	Ripening banana pu
7	536.5	66.5	724	19 AAV28660	Ripening banana pu
8	510.8	63.4	704	20 AAV69466	Banana fruit ripe
9	496.8	61.6	706	20 AAV69458	Banana fruit ripe

PS	Claim 1: Page 26; 72pp; English.
XX	The present sequence represents a cDNA clone isolated from ripening banana pulp. 57 clones were isolated and are given in AAV28643 to AAV28699. The cDNA clone sequences can be used in a method of modulating ripening or tissue senescence process in plants of the genus <i>Musa</i> . The method comprises: (a) inserting into the plant material at least 1 of the 57 sequences (as above); (b) regenerating the plant material, and (c) selecting from the transformed regenerants, plants with modulated ripening or tissue senescence characteristics. Also described in the present invention are: (1) plants, their progeny, seed and material obtained from the plants, produced by the above method; (2) a vector functional in plants comprising a promoter region which is operably in plant cells, a polynucleotide sequence as defined above, and a transcription termination sequence; and (3) a method of controlling plant pathogens comprising the application of anti-pathogenic agent to plants of (1).
XX	Sequence 806 BP; 157 A; 229 C; 212 G; 180 T; 28 other;
SQ	Query Match 96.5%; Score 778; DB 19; Length 806; Best Local Similarity 100.0%; Pred. No. 1e-221; Mismatches 0; Indels 0; Gaps 0 Matches 806; Conservative 0; Mismatches 0; Indels 0; Gaps 0 Qy 1 TGTTCCTCTCCCTCGATCACATCTTGTCTCTGGAAACCTGAGAGGTGAGACGGGGG 60 Db 1 TGTTCTCTCTCTCGATCACATCTTGTCTCTGGAAACCTGAGAGGTGAGACGGGGG 60 Qy* 61 GCAATGACGGGGGTTAAGTGGATTCTCTCTCTCTCTCTGGCTCTGGCTCTGGCTCTG 120 Db 61 GCAATGACGGGGGTTAAGTGGATTCTCTCTCTCTCTGGCTCTGGCTCTGGCTCTG 120 Qy 121 CTGGTTTGACGGAGTCGGGGGATGGAGCTGGGGGGATGGAGAGGGTCCCTCTGGCTCTGAGAAT 180 Db 121 CTGGTTTGACGGAGTCGGGGGATGGAGCTGGGGGGATGGAGAGGGTCCCTCTGGCTCTGAGAAT 180 Qy 181 GGCAGGATCGCGAGGAGCTGGAGAGGAGCTGGAGAGGAGCTGGAGAGGGCTCTGGAGAAT 240 Db 181 GGCAGGATCGCGAGGAGCTGGAGAGGAGCTGGAGAGGGCTCTGGAGAATGGCTCTGGAGAAT 240 Qy 241 TCCCTGAGAGAGGGCTGTRACCCGGGACAGAACGGGGACTGAGCAGAGGGCTCTGGCTCTGGAGAAT 300 Db 241 TCCCTGAGAGAGGGCTGTRACCCGGGACAGAACGGGGACTGAGCAGAGGGCTCTGGCTCTGGAGAAT 300 Qy 301 GTTGCTCGAGGGTCTGATGACCAATAATCACAGACGGCTCGAGATCTCTGGTAT 360 Db 301 GTTGCTCGAGGGTCTGATGACCAATAATCACAGACGGCTCGAGATCTCTGGTAT 360 Qy 361 CTGTCGTGCGGTCTGGCAACCCGATGAGCACTCTGGGGTGGACCCCTGATGGCAT 420 Db 361 CTGTCGTGCGGTCTGGCAACCCGATGAGCACTCTGGGGTGGACCCCTGATGGCAT 420 Qy 421 GTCACAGAGAGAAACCTCGTGACTGGGGCTTGGCTTGAGCCACGCAACGNATANGTGGC 480 Db 421 GTCACAGAGAGAAACCTCGTGACTGGGGCTTGGCTTGAGCCACGCAACGNATANGTGGC 480 Qy 481 CGCGACGGGAATTCTCTCGTGACAGACTCCGGGACAGATGCCCTTGAGCAACGCAACGNATANGTGGC 540 Db 481 CGCGACGGGAATTCTCTCGTGACAGACTCCGGGACAGATGCCCTTGAGCAACGCAACGNATANGTGGC 540 Qy 541 GCGCGGAACACTTANATACCCGCTNTCAANGAGTTCGCCCTCTGGATCCCTT 600 Db 541 GCGCGGAACACTTANATACCCGCTNTCCANGAGTTCGCCCTCTGGATCCCTT 600 Qy 601 AACACNAANTGGAATCTCNCCTCANGGAGAACTNTATGAACAGCTTAAACNAT 660 Db 601 AACACNAANTGGAATCTCNCCTCANGGAGAACTNTATGAACAGCTTAAACNAT 660 Qy 661 CGATGACGACNGTGTCTCGTCCACATGGCAATGCGCCCTGCTACCAACNCAATTTC 720 Db 661 CGATGACGACNGTGTCTCGTCCACATGGCAATGCGCCCTGCTACCAACNCAATTTC 720

XX	Sequence 724 BP; 143 A; 201 C; 197 G; 155 T; 28 other;
QY	481 CCGGACGCGGAATTGTGTTGTTGAGACATCGGGGACATGATCCCCGAAATCCTC 540 540
DB	488 CGGCACNGGGANTGTGNTGTTGTTGAGACATCGGGGACATGATCCCCGAAATCCTC 546 546
QY	541 GCGGGGACACTANATAACCCGTCWYCAANGAAGTGTGCCCTTGGAATCCCTT 600 600
DB	547 CCGGGAACACTTAAATTCGGTCATCCAG---ANCTNCCTCTGGATCNCCCTT 603 603
QY	601 AACNCNANTGGAAATCTCNCITCNANGAAGACTNTATGACAGCTTAANAGAT 660 660
DB	604 AACACGCAATGGAA-ATCNCACCCNGAAGAACTCCCTTAAACGGCTTNAACATC 662 662
QY	661 CGATGGACNCNGTGTCTCGTCCACATGGCAATGSGCCTGCTACANCAATTTCN 720 720
DB	663 NATGGACNCIGTCCACNTTCCACNTTGCCTATGGCCCTGCCTNCANCNATTA 722 722
QY	721 TCCCC 725 725
DB	723 TCNCC 727 727
RESULT 7	
ID	AAV28660 standard; cDNA; 724 BP.
XX	AAV28660;
AC	AAV28660;
XX	29-JUL-1998 (first entry)
DE	Ripening banana pulp cDNA clone U-0117 SEQ ID NO:18.
XX	Banana; ripening; pulp; Musa acuminata cv. Grand Nain; fruit; genetic control; tissue senescence; ss.
OS	Musa acuminata.
XX	W09811228-A2.
KW	Banana; ripening; pulp; Musa acuminata cv. Grand Nain; fruit; genetic control; tissue senescence; ss.
XX	08-SEP-1997; 97WO-GB02424.
PN	25-APR-1997; 97GB-0008366.
PR	10-SEP-1996; 96GB-0018862.
XX	(ZENE) ZENECA LTD.
XX	Bird CR, Medina-Suarez RDJ, Seymour GB;
DR	WPI; 1998-207389/18.
XX	Modulation of ripening or tissue senescence in bananas - comprises use of DNA isolated from ripening banana pulp to produce genetically modified fruit
XX	Claim 1; Page 29; 72pp; English.
PS	RESULT 8
ID	AAV69446 standard; cDNA; 704 BP.
XX	AAV69446;
AC	AAV69446;
XX	15-MAR-1999 (first entry)
DE	Banana fruit ripening-related clone U-12 cDNA.
XX	Fruit ripening; banana; modulator; tissue senescence; crop; plant; triploid; plant breeding; ss.
OS	Musa acuminata.
XX	W0953085-A1.
PN	W0953085-A1.

187	GCGGAGCATCGGGAGGGAGCTTGGAGAGGGCTTCCGGGACGCGGCGATGCTT	246	PR	PR	30-APR-1999;	9905-01324485
QY			PR	PR	04-MAY-1999;	9905-0132485
242	CCTTGGAAGAGGGCTGTAAACCGGGAGCAGAGCGCCAGTCGACCCGGAGGGAG	301	PR	PR	05-MAY-1999;	9905-0132485
247	CCTTGGAAGAGGGCTGTAAACCGGGAGCAGAGCGCCAGTCGACCCGGAGGGAG	306	PR	PR	06-MAY-1999;	9905-0132486
Db			PR	PR	07-MAY-1999;	9905-0132487
302	TCTCTTCGACGGGCTGTAGGACCATATACTAACACAGCACCGCTCCAGAGCTCTGGTTATC	361	PR	PR	11-MAY-1999;	9905-0132863
307	TCTCTTCGACGGGCTGTAGGACCATATACTAACACAGCACCGCTCCAGAGCTCTGGTTATC	366	PR	PR	14-MAY-1999;	9905-0134218
Db			PR	PR	14-MAY-1999;	9905-0134219
362	TGCTGTGGGTCAGGCACCCGGATCAGACTGCTGAGCTGCTGCGGSGTGCAGACCGGATGGCA	419	PR	PR	14-MAY-1999;	9905-0134421
Qy			PR	PR	14-MAY-1999;	9905-0134431
Db			PR	PR	18-MAY-1999;	9905-0134768
367	TGCTGTGGGTCAGGCACCCGGATCAGACTGCTGAGCTGCTGCGGSGTGCAGACCGGATGGCA	426	PR	PR	19-MAY-1999;	9905-0134941
Qy			PR	PR	20-MAY-1999;	9905-0135124
420	TGTCACACGAAAGAGCTGCTGACTGGGCATGTC-TTGGACGCCACGWNATNSTG	478	PR	PR	21-MAY-1999;	9905-0135353
427	TGTCACACGAAAGAGCTGCTGACTGGGCATGCTGTTGGCCGANCWNATATGT	486	PR	PR	24-MAY-1999;	9905-0135629
Db			PR	PR	25-MAY-1999;	9905-0136021
Qy			PR	PR	27-MAY-1999;	9905-0136392
479	GCGCC-GACGSGGATTTGTTGTTG-TGACAGATCC-GGGACGATGATCCCCTG	534	PR	PR	28-MAY-1999;	9905-0136782
487	GGCGCAGCGGGGAGNATGTTGCTGTTGACANACTCGGGGAGATCCGGGAGATCCGGGAA	546	PR	PR	01-JUN-1999;	9905-0137228
535	ATCCCTCGCC-GGGACACTANATACCCGTCNTCAANGAGTGGCCCTCTGGGA	592	PR	PR	03-JUN-1999;	9905-0137528
Qy			PR	PR	04-JUN-1999;	9905-0137502
547	ATCCTCCCCGCGGGAACTTANATCNCCTGATCAGACCTTANATCNCCTGATCAGACCTT	603	PR	PR	07-JUN-1999;	9905-0137724
Db			PR	PR	08-JUN-1999;	9905-0138074
Qy			PR	PR	10-JUN-1999;	9905-0138540
593	TCCCTTTAACNCNAANGGAAATCTCNCTCNAANGGAAACTCTNTATGAAAGCCTT	652	PR	PR	10-JUN-1999;	9905-0138847
Qy			PR	PR	14-JUN-1999;	9905-0139119
604	TCCCTTTAACNCNAANGGAAATCACCTCC-NGANGAAACTCTCTPATGAAACA-CTTT	661	PR	PR	16-JUN-1999;	9905-0139452
Qy			PR	PR	17-JUN-1999;	9905-0139453
653	AAACACATCGATGAGCAGCAGNGTGCCTCTCCACATGCCAATGGC	697	PR	PR	18-JUN-1999;	9905-0139454
Db			PR	PR	18-JUN-1999;	9905-0139455
662	AAACACATCCAGGNCNCNGTGTCACTGACATTTGCCNATGGC	706	PR	PR	18-JUN-1999;	9905-0139456
RESULT 10			PR	PR	18-JUN-1999;	9905-0139458
AC36622	AC36622 standard; DNA; 1633 BP.		PR	PR	18-JUN-1999;	9905-0139458
AC	AC36622;		PR	PR	18-JUN-1999;	9905-0139458
XX			PR	PR	18-JUN-1999;	9905-0139458
DT	17-OCT-2000 (first entry)		PR	PR	18-JUN-1999;	9905-0139458
XX			PR	PR	18-JUN-1999;	9905-0139458
DE	Arabidopsis thaliana DNA fragment SEQ ID NO: 14477.		PR	PR	18-JUN-1999;	9905-0139458
XX			PR	PR	18-JUN-1999;	9905-0139458
KW	Hybridisation assay; genetic mapping; gene expression control;		PR	PR	18-JUN-1999;	9905-0139458
KW	protein identification; signal transduction pathway;		PR	PR	18-JUN-1999;	9905-0139458
KW	metabolic pathway; promoter; termination sequence; ss.		PR	PR	18-JUN-1999;	9905-0139458
XX			PR	PR	18-JUN-1999;	9905-0139458
OS	Arabidopsis thaliana.		PR	PR	18-JUN-1999;	9905-0139458
XX			PR	PR	18-JUN-1999;	9905-0139458
PN	EP1033405-A2.		PR	PR	18-JUN-1999;	9905-0139458
XX			PR	PR	18-JUN-1999;	9905-0139458
PD	06-SEP-2000.		PR	PR	18-JUN-1999;	9905-0139458
XX			PR	PR	18-JUN-1999;	9905-0139458
PF	25-FEB-2000; 2000EP-0301439.		PR	PR	18-JUN-1999;	9905-0139458
PR	25-FEB-1999; 9905-0121825.		PR	PR	18-JUN-1999;	9905-0139458
PR	05-MAR-1999; 9905-0123180.		PR	PR	18-JUN-1999;	9905-0139458
PR	09-MAR-1999; 9905-0123548.		PR	PR	18-JUN-1999;	9905-0139458
PR	23-MAR-1999; 9905-0125788.		PR	PR	18-JUN-1999;	9905-0139458
PR	25-MAR-1999; 9905-0126264.		PR	PR	18-JUN-1999;	9905-0139458
PR	29-MAR-1999; 9905-0126785.		PR	PR	18-JUN-1999;	9905-0139458
PR	01-APR-1999; 9905-0127462.		PR	PR	18-JUN-1999;	9905-0139458
PR	06-APR-1999; 9905-0128234.		PR	PR	18-JUN-1999;	9905-0139458
PR	08-APR-1999; 9905-0128714.		PR	PR	18-JUN-1999;	9905-0139458
PR	16-APR-1999; 9905-0129845.		PR	PR	18-JUN-1999;	9905-0139458
PR	19-APR-1999; 9905-0130077.		PR	PR	18-JUN-1999;	9905-0139458
PR	21-APR-1999; 9905-0130449.		PR	PR	18-JUN-1999;	9905-0139458
PR	23-APR-1999; 9905-0130510.		PR	PR	18-JUN-1999;	9905-0139458
PR	23-APR-1999; 9905-0130891.		PR	PR	18-JUN-1999;	9905-0139458
PR	28-APR-1999; 9905-0131449.		PR	PR	18-JUN-1999;	9905-0139458
PR	30-APR-1999; 9905-0132048.		PR	PR	18-JUN-1999;	9905-0139458

PR	21-JUL-1999;	99US-0145088.	PR	21-OCT-1999;	99US-0160767.
PR	22-JUL-1999;	99US-0145085.	PR	21-OCT-1999;	99US-0160768.
PR	22-JUL-1999;	99US-0145087.	PR	21-OCT-1999;	99US-0160814.
PR	22-JUL-1999;	99US-0145089.	PR	21-OCT-1999;	99US-0160815.
PR	23-JUL-1999;	99US-0145145.	PR	22-OCT-1999;	99US-0160981.
PR	23-JUL-1999;	99US-0145218.	PR	22-OCT-1999;	99US-0160981.
PR	26-JUL-1999;	99US-0145224.	PR	22-OCT-1999;	99US-0160989.
PR	27-JUL-1999;	99US-0145276.	PR	25-OCT-1999;	99US-0161404.
PR	27-JUL-1999;	99US-0145913.	PR	25-OCT-1999;	99US-0161405.
PR	27-JUL-1999;	99US-0145918.	PR	25-OCT-1999;	99US-0161406.
PR	28-JUL-1999;	99US-0145931.	PR	26-OCT-1999;	99US-0161360.
PR	02-AUG-1999;	99US-0146386.	PR	26-OCT-1999;	99US-0161361.
PR	02-AUG-1999;	99US-0146389.	PR	28-OCT-1999;	99US-0161920.
PR	03-AUG-1999;	99US-0147038.	PR	28-OCT-1999;	99US-0161921.
PR	04-AUG-1999;	99US-0147204.	PR	28-OCT-1999;	99US-0161993.
PR	04-AUG-1999;	99US-0147302.	PR	29-OCT-1999;	99US-0162142.
PR	05-AUG-1999;	99US-0147192.			
PR	05-AUG-1999;	99US-0147260.			
PR	06-AUG-1999;	99US-017303.			
PR	09-AUG-1999;	99US-0147416.			
PR	09-AUG-1999;	99US-014793.			
PR	10-AUG-1999;	99US-0148117.			
PR	11-AUG-1999;	99US-0148319.	Db	243	GRACATGCGATGAGAACCCAGATGAGTCGAGCTGCGCCAGTGGAGCAGACATTCGAAAC 302
PR	12-AUG-1999;	99US-0148341.	Qy	334	AGCACGGCTCGAGATCTTGTGTTATCTCTGTGGCTGGTTCAGGCAACCGGATCAGAC 393
PR	13-AUG-1999;	99US-0148505.	Db	303	ASCCACAGCAGCAGAACGATAGTAGTACGTTACGTTCTGCACCGGACCGGAAACCCGAGAT 362
PR	13-AUG-1999;	99US-0148634.	Qy	454	GGTTTGGACGCAAGCAGTAAAGTGGCGGAGGGAATTGTCCTGTCAGCACAGCT 513
PR	16-AUG-1999;	99US-0149368.	Db	423	GGATTGTCGGCACCGCATCGGGCGCGAC-GGGTGTCTACGTTGTAACCGAAC 481
PR	17-AUG-1999;	99US-0149115.	Qy	394	TGCTGGCGTGGACCCCTGATGGCAGTCACAGAAAAAGCTCGCTGACTGGCATT 453
PR	18-AUG-1999;	99US-0149426.	Db	363	TGCTGGCGTGGACCCGAATGGCAGTCGGTGCACCGGAAACGGTACGGATGCTCAGTCATC 422
PR	20-AUG-1999;	99US-0149722.			
PR	20-AUG-1999;	99US-0149723.			
PR	20-AUG-1999;	99US-0149939.			
PR	23-AUG-1999;	99US-0149902.			
PR	23-AUG-1999;	99US-0149930.			
PR	25-AUG-1999;	99US-0150566.			
PR	26-AUG-1999;	99US-0150884.	Qy	514	CGGGGACAGATGATCCCCGTGAATCTCTGCCCGGGAACTTAATACCCGTCNTCAA 573
PR	27-AUG-1999;	99US-0151065.	Db	482	TGCGAGGACGAT-CCGGTAACTCCATACCGGGACACTTACCGGCGATCCTGTCAGCCGATTC- 537
PR	27-AUG-1999;	99US-0151066.	Qy	574	GAAGTTGCCCTCTGGATCCCTTAAACNCNAACTCTCNCTCNANGGAAGA 633
PR	30-AUG-1999;	99US-0151303.	Db	538	AAGACGAGAACCTCTGGATCATCTTCACACGGACATGGTTAAAC-CTTGAAAGCAGA 595
PR	31-AUG-1999;	99US-0151438.			
PR	01-SEP-1999;	99US-0151930.			
PR	07-SEP-1999;	99US-0152363.			
PR	10-SEP-1999;	99US-0153070.	Qy	634	ACTCTNTATGAGCAGCTTAANACNATGAGCAGCAGNCNGTGTCTGTCACATGCCAA 693
PR	13-SEP-1999;	99US-0153758.	Db	596	GCCTGATCATGAAACGCTTCACACCATGATGGTCTGGTGTCAATGTTACATCGCTAA 655
PR	15-SEP-1999;	99US-0154018.			
PR	16-SEP-1999;	99US-0154039.			
PR	20-SEP-1999;	99US-0154779.	Qy	694	TGGCCCTGCGNTCAACCNAATTCTWCWCCACACNCCTCTCCTCNCWNGCCCTCC 752
PR	22-SEP-1999;	99US-0155139.	Db	656	TGAGCTGTCACGATCAATGAGTACGACATATTGTCATGGATTCATGTC 714
PR	23-SEP-1999;	99US-0155486.			
PR	24-SEP-1999;	99US-0155659.			
PR	28-SEP-1999;	99US-0156458.			
PR	29-SEP-1999;	99US-0156536.			
PR	04-OCT-1999;	99US-0157117.	RESULT 11		
PR	05-OCT-1999;	99US-015753.	AAV69449		
PR	06-OCT-1999;	99US-0157865.	ID	AAV69449 standard; cDNA; 823 BP.	
PR	07-OCT-1999;	99US-0158029.	XX		
PR	08-OCT-1999;	99US-0158232.	AC	AAV69449;	
PR	12-OCT-1999;	99US-0158369.	XX		
PR	13-OCT-1999;	99US-0159293.	DT	15-MAR-1999 (first entry)	
PR	13-OCT-1999;	99US-015924.	XX		
PR	13-OCT-1999;	99US-015925.	DE	Banana fruit ripening-related clone U-51 cDNA.	
PR	14-OCT-1999;	99US-0159329.	XX		
PR	14-OCT-1999;	99US-0159331.			
PR	14-OCT-1999;	99US-0159637.			
PR	14-OCT-1999;	99US-0159638.			
PR	18-OCT-1999;	99US-0159584.			
PR	21-OCT-1999;	99US-0160741.	OS	Musa acuminata.	
PR	21-OCT-1999;	99US-0160741.	XX		
PR	21-OCT-1999;	99US-0160767.	PN	W09853085-A1.	
PR	21-OCT-1999;	99US-0160768.	XX		
PR	21-OCT-1999;	99US-0160814.			
PR	21-OCT-1999;	99US-0160815.			
PR	22-OCT-1999;	99US-0160981.			
PR	22-OCT-1999;	99US-0160981.			
PR	22-OCT-1999;	99US-0160981.			
PR	22-OCT-1999;	99US-0161359.			
PR	26-OCT-1999;	99US-0161360.			
PR	26-OCT-1999;	99US-0161361.			
PR	28-OCT-1999;	99US-0161920.			
PR	28-OCT-1999;	99US-0161921.			
PR	28-OCT-1999;	99US-0161993.			
PR	29-OCT-1999;	99US-0162142.			
			Query	Match	Score 169.4; DB 21; Length 1633;
			Best local	Similarity	21.0%; Score 169.4; DB 21; Length 1633;
			Matches	304;	Pred. No 4 6e-40; Mismatches 169; Indels 7; Gaps 4;
			Qy	274	GAAGCCGAGTGCAGACGACCCAGAGGAGATGCTGAGTGGCTGTTGAGCCTAATCAC 333
			Db	243	GRACATGCGATGAGAACCCAGATGAGTCGAGCTGCGCCAGTGGTGAACGAGCATTCGAAAC 302
			Qy	334	AGCACGGCTCGAGATCTTGTGTTATCTCTGTGGCTGGTTCAGGCAACCGGATCAGAC 393
			Db	303	ASCCACAGCAGCAGAACGATAGTAGTACGTTCTGCACCGGACCGGAAACCCGAGAT 362
			Qy	454	GGTTTGGACGCAAGCAGTAAAGTGGCGGAGGGAATTGTCCTGTCAGCACAGCT 513
			Db	423	GGATTGTCGGCACCGCATCGGGCGCGAC-GGGTGTCTACGTTGTAACCGAAC 481
			Qy	574	GAAGTTGCCCTCTGGATCCCTTAAACNCNAACTCTCNCTCNANGGAAGA 633
			Db	538	AAGACGAGAACCTCTGGATCATCTTCACACGGACATGGTTAAAC-CTTGAAAGCAGA 595
			Qy	634	ACTCTNTATGAGCAGCTTAANACNATGAGCAGCAGNCNGTGTCTGTCACATGCCAA 693
			Db	596	GCCTGATCATGAAACGCTTCACACCATGATGGTCTGGTGTCAATGTTACATCGCTAA 655
			Qy	694	TGGCCCTGCGNTCAACCNAATTCTWCWCCACACNCCTCTCCTCNCWNGCCCTCC 752
			Db	656	TGAGCTGTCACGATCAATGAGTACGACATATTGTCATGGATTCATGTC 714

XX	26-NOV-1998.	98WO-GB01297.
XX	Hybridisation assay; genetic mapping; gene expression control	
PR	protein identification; signal transduction pathway;	
XX	metabolic pathway; promoter; termination sequence; ss.	
PA	(ZENE) ZENeca LTD.	
XX		
PT	Bird CR, Medina-Suarez RDJ, Seymour GB;	
XX		
DR	WPI; 1999-059745/05.	
XX		
PT	New method of modulating fruit ripening or tissue senescence characteristics of Musa plants - by introducing DNA sequences, useful in processes for modifying plant/fruit ripening	
PT	characteristics	
XX		
PS	Claim 1; Page 24: 78pp; English.	
XX		
CC	AAV69440-V6512 are cDNA sequences which are used in a method to modulate the fruit ripening or tissue senescence characteristics of Musa acuminate (banana) plants. The method provides a recombinant way of modulating ripening/senescence characteristics of bananas, which are a globally important crop. In particular, the method can modulate such characteristics in the dessert banana, which due to its triploid nature is unaffected by conventional plant breeding techniques.	
CC	sequence 823 BP; 168 A; 266 C; 222 G; 150 T; 17 other;	
SQ	Query Match 18.7%; Score 151; DB 20; Length 823; Best Local Similarity 63.7%; Pred. No. 1.le-34; Matches 272; Conservative 0; Mismatches 149; Indels 6; Gaps 4; Matches 272; Conservative 0; Mismatches 149; Indels 6; Gaps 4;	
Qy	327 ARTCAACACGCCCTCGCAGATCTCTGGTTATCTGTCGGCGGTTCAGCAACCGAT 386	PR 30-APR-1999; 99US-0132048.
Db	137 AAGCTTGAGCTGAGCTGCGCGGGGAGCTGGGCTACTTGTCTGCGCACCGCAATCCGAT 196	PR 04-MAY-1999; 99US-0132484.
Qy	387 CGACGACGCTGCGGCGTGCACGACCTGATGGCAGTCACAGAALAAACTCTGGTACTG 446	PR 05-MAY-1999; 99US-0132485.
Db	197 CGACGACTCTGGCGGTGCGATCTGACTGGGCGACACCGCGAGCGGCTCGGGACTG 256	PR 06-MAY-1999; 99US-0132486.
Qy	447 CGCGCATTCGGCTTGACCCNACTGTCGGCGGAGATTTGTTGCTGTGTA 506	PR 07-MAY-1999; 99US-0132833.
Db	257 CGCCATTCGGGTTGGAAAGAACCGGATGGGGGGAGGGCG-AGATATACGGTGTGA 315	PR 11-MAY-1999; 99US-0134256.
Qy	507 CAGACTCGGGGACNATGATCCCGGTGATCTGGCCCGGAACACTTANATACCCCGTC 566	PR 14-MAY-1999; 99US-0134219.
Db	316 CGGACGAGGGCACGACCA-CCCGTCAACATCGGAGCGGGCACCGTCCGGTAGCCGCG 374	PR 14-MAY-1999; 99US-0134221.
Qy	567 ATGCCAAGAAGTGTGCCCTCTGGATCCCTTAACACNAATGGAAATCTCTCTNA 626	PR 18-MAY-1999; 99US-0134370.
Db	375 ATCCAGGGAGGCCGCTGT--GGATCATCTCAAGCGGACATGGTATC-GAGTTGA 430	PR 19-MAY-1999; 99US-013441.
Qy	627 NGGAAAGACTCNNTATGACAGCTTAANACNATCGATGAGCAGCNGNGTGCCTCTCCACA 686	PR 20-MAY-1999; 99US-0135124.
Db	431 ATGGAGGAGCTCATCATGACTCCCAACGACCATGAGGGCGGGCGCAGCTCCACA 490	PR 21-MAY-1999; 99US-013533.
Qy	687 TTGCCCAATGGCGCTGCNTCCACGCCATTTCNTCCACNTCTTCCTCCTNNGCCCTC 746	PR 24-MAY-1999; 99US-0135529.
Db	491 TCCTCGGGGGCGGTGATCACCATCCAGTAGTCACACATCATCCTACCCAGGGCGC 550	PR 25-MAY-1999; 99US-0136021.
Qy	747 CAGTCCTC 753	PR 27-MAY-1999; 99US-0136332.
Db	551 CACATCC 557	PR 28-MAY-1999; 99US-0136782.
RESULT 12		PR 01-JUN-1999; 99US-013722.
AAC42069		PR 03-JUN-1999; 99US-0137528.
ID	AAC42069 standard; DNA; 1526 BP.	PR 04-JUN-1999; 99US-0137702.
XX		PR 04-JUN-1999; 99US-0137724.
AC	AAC42069;	PR 08-JUN-1999; 99US-0138094.
XX		PR 10-JUN-1999; 99US-0138340.
PR		PR 10-JUN-1999; 99US-0138450.
PR		PR 14-JUN-1999; 99US-0139119.
PR		PR 16-JUN-1999; 99US-0139452.
PR		PR 16-JUN-1999; 99US-0139453.
PR		PR 17-JUN-1999; 99US-0139492.
PR		PR 18-JUN-1999; 99US-0139454.
PR		PR 18-JUN-1999; 99US-0139455.
PR		PR 18-JUN-1999; 99US-0139456.
PR		PR 18-JUN-1999; 99US-0139457.
PR		PR 18-JUN-1999; 99US-0139458.
PR		PR 18-JUN-1999; 99US-0139459.
PR		PR 18-JUN-1999; 99US-0139460.
PR		PR 18-JUN-1999; 99US-0139461.
PR		PR 18-JUN-1999; 99US-0139462.
PR		PR 18-JUN-1999; 99US-0139463.
PR		PR 18-JUN-1999; 99US-0139750.
PR		PR 18-JUN-1999; 99US-0139763.

PR	21-JUN-1999;	99US-0139899.
PR	22-JUN-1999;	99US-0151303.
PR	23-JUN-1999;	99US-0140354.
PR	24-JUN-1999;	99US-0140695.
PR	28-JUN-1999;	99US-0140823.
PR	29-JUN-1999;	99US-0140991.
PR	30-JUN-1999;	99US-0141287.
PR	01-JUL-1999;	99US-0141842.
PR	01-JUL-1999;	99US-0142154.
PR	02-JUL-1999;	99US-0142055.
PR	15-JUL-1999;	99US-0142390.
PR	08-JUL-1999;	99US-0142803.
PR	09-JUL-1999;	99US-0142920.
PR	12-JUL-1999;	99US-0142977.
PR	13-JUL-1999;	99US-0143542.
PR	14-JUL-1999;	99US-0143624.
PR	15-JUL-1999;	99US-0144005.
PR	16-JUL-1999;	99US-0144085.
PR	16-JUL-1999;	99US-0144086.
PR	19-JUL-1999;	99US-0144325.
PR	19-JUL-1999;	99US-0144331.
PR	19-JUL-1999;	99US-0144332.
PR	19-JUL-1999;	99US-0144333.
PR	19-JUL-1999;	99US-0144334.
PR	19-JUL-1999;	99US-0144335.
PR	20-JUL-1999;	99US-0144352.
PR	20-JUL-1999;	99US-0144632.
PR	20-JUL-1999;	99US-0144884.
PR	21-JUL-1999;	99US-0144814.
PR	21-JUL-1999;	99US-0145086.
PR	21-JUL-1999;	99US-0145224.
PR	22-JUL-1999;	99US-0145085.
PR	22-JUL-1999;	99US-0145276.
PR	22-JUL-1999;	99US-0145913.
PR	22-JUL-1999;	99US-0145089.
PR	22-JUL-1999;	99US-0145192.
PR	23-JUL-1999;	99US-0145145.
PR	23-JUL-1999;	99US-0145218.
PR	23-JUL-1999;	99US-014551.
PR	26-JUL-1999;	99US-0145224.
PR	26-JUL-1999;	99US-0145386.
PR	02-AUG-1999;	99US-0146388.
PR	02-AUG-1999;	99US-0146389.
PR	03-AUG-1999;	99US-0147038.
PR	04-AUG-1999;	99US-0147204.
PR	04-AUG-1999;	99US-0147302.
PR	05-AUG-1999;	99US-0147192.
PR	05-AUG-1999;	99US-0147260.
PR	06-AUG-1999;	99US-0147303.
PR	06-AUG-1999;	99US-0147415.
PR	09-AUG-1999;	99US-0147493.
PR	09-AUG-1999;	99US-0147495.
PR	10-AUG-1999;	99US-0147935.
PR	11-AUG-1999;	99US-0148319.
PR	12-AUG-1999;	99US-0148341.
PR	13-AUG-1999;	99US-0148565.
PR	13-AUG-1999;	99US-0148684.
PR	16-AUG-1999;	99US-0149368.
PR	17-AUG-1999;	99US-0149175.
PR	18-AUG-1999;	99US-0149426.
PR	20-AUG-1999;	99US-0149722.
PR	20-AUG-1999;	99US-0149723.
PR	20-AUG-1999;	99US-0149929.
PR	23-AUG-1999;	99US-0149902.
PR	23-AUG-1999;	99US-0149930.
PR	25-AUG-1999;	99US-0150566.
PR	26-AUG-1999;	99US-0150884.
PR	27-AUG-1999;	99US-0151065.
PR	27-AUG-1999;	99US-0151066.
QY	274	GAAGCCGCAGTCGAGCCGGAGGGAGGTTGCTTGACGCCCTGTATGACCCATATCAC
Db	203	GAACATGCACTTGAGATCTCTGGTATCGTGCGGGTTAGGAGTACTGCCATGGACATGGACATCGAAC
QY	334	AGCAGGGCTCGAGATCTCTGGTATCGTGCGGGTTAGGAGAATCCACGGAAATCCACGGATCGAC
Db	263	AGCACAGGAGAGATAGGATCTCATCCTCAACGGAAATCCACGGATCGACATCGACAT
QY	394	TGCTGGGGTGCAGCCGCTGATGGATGTCACAGAAAAGCTGCTGACTGGCAT
Db	323	TGTTGGGTTGTGATGGAGATGGCAATCCGGCAAAACATCTAGGCCATTGGCAATC
QY	454	GCCTTGAGCCAAAGCNATANGTGGCCGGACGGGAATTGTTGTTGACAGACTC
Db	383	GGGGTCGGCGCAAGCAATCGGAGGCCGAGAC GGTCTTACTTGTAGTGTGACCC
QY	514	CGGGCAGNATGATCCCGTGATCTCGGCCGGACACTTANATACCCGTCWCCAAN
Db	442	AACACGATACCGGTTATCCCTAAACCGGGGACATTAAGTCGACGAAATTAATCAAG

Qy 574 GAAGTGTCCCTCTGGATCCCTTAACNCNAANTGGAATCTCNCICNANGAAGA 633
 Db 502 AA---GAACATTATGGACGCTTAAACGTGACATGCA-ATAAGAAGA 556
 Qy 634 ACTCNNTATGACAGCTTAAACNATCAGTGGACNGTCCCTGTCACATGCCAA 693
 Db 557 ACTAATCATGACAGTTCAACACATGATGGCTGGTCACATRGCTAA 616
 Qy 694 TGGCCTGTGTCACCCAAATTCTNTCCCAACTTCTTCNTGCTCCNCTCCC 753
 Db 617 TGGTACATGATCAGTCACTGAGTGTGACATACATTCAGGAAATCATATCA 676
 Qy 754 CAAT 757
 Db 677 TGAT 680

RESULT 13
 AAV9445
 ID AAV9445 standard; cDNA; 749 BP.
 XX AAV9445;
 XX DT 15-MAR-1999 (first entry)
 DE Banana fruit ripening-related clone U-11 cDNA.
 XX KW Fruit ripening; banana; modulator; tissue senescence; crop; plant;
 KW triploid; plant breeding; ss.
 XX OS Musa acuminata.
 XX PN WO9853085-A1.
 XX PD 26-NOV-1998.
 XX PF 05-MAY-1998; 98WO-GB01297.
 XX PR 20-MAY-1997; 97GB-0010370.
 XX PA (ZENE) ZENECA LTD.
 XX PI Bird CR, Medina-Suarez RDJ, Seymour GB;
 XX WPI; 1999-059745/05.

PT New method of modulating fruit ripening or tissue senescence characteristics of Musa plants - by introducing DNA sequences, useful in processes for modifying plant/fruit ripening characteristics
 XX PS Claim 1; Page 21-22; 78pp; English.

XX AAV9440-W69512 are cDNA sequences which are used in a method to modulate the fruit ripening or tissue senescence characteristics of Musa acuminata (banana) plants. The method provides a recombinant way of modulating ripening/senescence characteristics of bananas, which are a globally important crop. In particular, the method can modulate such characteristics in the dessert banana, which due to its triploid nature is unaffected by conventional plant breeding techniques.

XX Sequence 749 BP; 157 A; 245 C; 197 G; 128 T; 22 other;
 CC Query Match 17.9%; Score 1444; DB 20; Length 749;
 CC Best Local Similarity 64.0%; Pred No. 9.4e-33;
 CC Matches 275; Conservative 0; Mismatches 147; Indels 8; Gaps 5;
 CC WPI; 1998-207389/18.

Qy 325 ATATCAACAGCAGGGCTCGAGATCTCTGGTATCTGCTGGGTCAGGGACCCG 384
 Db 135 AGAAGCTTGAACGTCGGCGGGCACTGGCTACTGTCATGGCACCGGAATCG 194
 Qy 385 ATCGAGCAGTCGGGGTGGACCCCTGATGGCATGAAACAGAAAGCTCGCTGAC 444

Db 195 ATCGAGCAGCTGGGGTGGACCCCTGACTGGGTGACACCGCGAGCGCTCCGTAC 254
 Qy 445 TCGGCATGGCTTGTGACGCCAACGCNATANGGGCGGAGGGAAATTGGTGTGTTG 504
 Db 255 TGGCCATCGGGTGGGAGACCGGGCAGGGACGGGG-AGATATGTT 313
 Qy 505 GACAGACTCCGGGAGATGATCCCGTGAATCTGGCCGGAAACTANATACCCG 564
 Db 314 GACCGACAGTGGCGAGACNA-CCCGGTCAATCCCAAAGGGCAGCTCGGTAAGCG 372
 Qy 565 TCNTCCAAANGAAGTTCGCCCTCTGGATCCCTTAAACNCNAANTGGAATCTCNC 624
 Db 373 TCATCC---AGGAGGAGCCCTGTTGATCATCTTAAGGGGACATGGTCATCCAGCTG 428
 Qy 625 NANGAAGA-CTCNCNTATCACACTTAAACNATCAGTGGACNGTCCPCTGTC 683
 Db 429 AAAGGAGGAGGAGCTCATGACTTCAACAGACCATGACGAGCCGGGGCCACAGCTC 488
 Qy 684 ACATGCCAATGGCCCTGCNTCACCCAAATTCTNTCCCACTCTCTCCNTGC 743
 Db 489 ACATCCCGGGGGCGTGCATCACATCC-AGTAGCTCACCAACATCNICATCCACGGC 547
 Qy 744 CTCCNCTCCC 753
 Db 548 GTCCACATCC 557

RESULT 14
 AAV28659 standard; cDNA; 842 BP.
 ID AAV28659
 XX AC AV28659;
 XX DT 29-JUL-1998 (first entry)
 DE Ripening banana pulp cDNA clone U-0115 SEQ ID NO:17.
 XX KW Banana; ripening; pulp; Musa acuminata cv. Grand Nain; fruit;
 KW genetic control; tissue senescence; ss.
 XX OS Musa acuminata.
 XX PN WO9811228-A2.
 XX PD 19-MAR-1998.
 XX PF 08-SEP-1997; 97WO-GB02424.
 XX PR 25-APR-1997; 97GB-0008366.
 XX PR 10-SEP-1996; 96GB-0018862.
 XX PA (ZENE) ZENECA LTD.
 XX PI Bird CR, Medina-Suarez RDJ, Seymour GB;
 XX WPI; 1998-207389/18.

PT Modulation of ripening or tissue senescence in bananas - comprises use of DNA isolated from ripening banana pulp to produce genetically modified fruit
 XX PS Claim 1; Page 28-29; 72pp; English.

CC The present sequence represents a cDNA clone isolated from ripening banana pulp. 57 clones were isolated and are given in AAV28643 to AAV28699. The cDNA clone sequences can be used in a method of modulating ripening or tissue senescence process in plants of the genus Musa. The method comprises: (a) inserting into the plant material at least 1 of the 57 sequences (as above); (b) regenerating the plant material; and (c) selecting from the transformed regenerants plants with modulated ripening or tissue senescence characteristics. Also described in the present invention are: (1) plants, their progeny, seed and material

CC obtained from the plants, produced by the above method; (2) a vector
 CC in plants comprising a promoter region which is operably in
 CC plant cells, a polynucleotide sequence as defined above, and a
 CC transcription termination sequence; and (3) a method of controlling
 CC plant pathogens comprising the application of anti-pathogenic agent to
 plants of (1).

XX Sequence 842 BP; 177 A; 277 C; 218 G; 154 T; 16 other;

Query Match 17.7%; Score 142.8; DB 19; Length 842;
 Best Local Similarity 64.3%; Pred. No. 3e-32; PT
 Matches 276; Conservative 0; Mismatches 144; Indels 9; Gaps 5; PT
 PT

QY 325 ATAAATCACACAGCACGGCTCGAGATCTCTGGTTATCTGTTGCGTGTAGGCCAACCG 384
 DB 140 AGAACGTTGACGTGCGCGCGGACTGGCTACTTGTCTATGCCGACCGAACCTCG 199
 QY 385 ATGAGACGACTGCTGGGGTGGGACCCGTGATGGCAGTCAACAGAAAAAGCTGCTGAC 444
 DB 200 ATGGACGACATGCTGGGGTGGGACCCGTGACTGGCTGACACCGCAGCGCTCGTGAC 259
 QY 445 TCGGGATTCGCTTGGACGGACCGNATANCTGGCCGACGGGAATTGTTGCTGT 504
 DB 260 TGGCCCATCGGGTGGGACAGAACAGCTGGGAGGACGGGACGGGAGGAGGCG-AGATACTGCTGAC 318
 QY 505 GACAGACTCCGGGAGCNAATGATGCCGGTGAATCTCGCCGGAGACCTANATACCCG 564
 DB 319 GACCGACAGTGGCAGACNAAGA-CCCCGTCATCCGAAACACGGCAGCTCCGGTAGCCG 377
 QY 565 TCNTCCANGAAGTGTGCCCTCTGGATTCCTAAACNATCGATGACAGCCTTAACNCAANTGAAATCNC 624
 DB 378 TCATCC---AGGAGGAGCCGCTGTGGATCATCTCTCAAGGCCACAGTGGCTCATCCAGCT- 432
 QY 625 NANGGAGAACTCTATGACAGCTTAACNATCGATGACAGCCTTAACNCAANTGAAATCNC 684
 DB 433 GAAGGGAGGACTCATGATGAACTCCACAAAGAACCATCGACGCCGCGGCGCAGGGCA 492
 QY 688 CATGGCAATGGCCCTGCNTACCCAAATTCTCCCGAACNCTCTCCNTNGCC 744
 DB 493 CATCTCGGGCGGCCGCTGACATCACC--AGTACCTCACCAACATCATTCACGGGG 550
 QY 745 TCCNCATCCC 753
 DB 551 TCCACATCC 559

DR WPI; 1999-059745/05.
 XX AA96940-v09512 are cDNA sequences which are used in a method to
 CC modulate the fruit ripening or tissue senescence characteristics of Musa
 CC acuminate (banana) plants. The method provides a recombinant way of
 CC modulating ripening/senescence characteristics of bananas, which are a
 CC globally important crop. In particular, the method can modulate such
 CC characteristics in the dessert banana, which due to its triploid nature
 CC is unaffected by conventional plant breeding techniques.

XX Sequence 708 BP; 140 A; 225 C; 192 G; 134 T; 17 other;

Query Match 17.5%; Score 141.4; DB 20; Length 708;
 Best Local Similarity 60.3%; Pred. No. 7.e-32; PT
 Matches 290; Conservative 0; Mismatches 182; Indels 9; Gaps 5; PT
 PT

QY 325 ATAAATCACACAGCACGGCTCGAGATCTCTGGTTATCTGTTGCGTGTAGGCCAACCG 384
 DB 137 AGAACGTTGACGTGCGGGCGGCGACTGGCTACTTGTCTATGCCGACCGGAAATCCG 196
 QY 385 ATGAGACGACTGCTGGGGTGGGACCCGTGATGGCAGTCAACAGAAAAAGCTGCTGAC 444
 DB 197 ATGAGACGACTGCTGGGGTGGGACCCGTGACTGGCTGACACCGCAGCGCTCGGGAC 256
 QY 445 TCGGGATTCGCTTGGACGGACCGNATANCTGGCCGACGGGAATTGTTGCTGTTG 504
 DB 257 TCGCCCATCGGGTCTGGGAGAACGCGATGGGGGANGGACGGG-ANATACTGTT 315
 QY 505 GACAGACTCCGGGAGCNAATGATGCCGGTGAATCTCGCCGGAGCGCTCATCCAGCTGAC 564
 DB 316 GACCGACAGTGGCAGACNA-CCCCGTCATCCGAAACCGCAGCGCTCGGTACGCCG 374
 QY 565 TCNTCCANGAAGTGTGCCCTCTGGATCCCTTAACNCAANTGAAATCNC 624
 DB 375 TCATCC---AGGAGGAGCCGCTGTGACATCATTCACGGGG 310
 QY 625 NANGGAGAACTCTATGACAGCTTAACNATCGATGACAGCCTTAACNCAANTGAAATCNC 684
 DB 431 AAGGGAGGACTCATCCGACCCACAGCTTACNCAACGCTGCTCC 490
 QY 685 CATGGCAATGGCCCTGCNTACCCAAATTCTCCCGAACNCTCTCCNTNGCC 743
 DB 491 CATCTCGGGGGCGCTGACATCCACCATCGAGTACTTGTCTCCACAGCTCAGGGC 550
 AC 744 CTCCNC---TCCCAATGACACCCNCCGGAAATTCTCTGCTCCCNCTCCCTCTCCATG 801
 DT XX 551 GTCACATCCAGGACTGCACTCCAGGGAAACCTCTGGTCCACCTCCATG 610
 DE Banana fruit ripening-related clone U-31 cDNA.
 XX
 KW Fruit ripening; banana; modulator; tissue senescence; crop; plant;
 KW triploid; plant breeding; ss.
 XX
 OS Musa acuminata.
 XX WO9853085-A1.
 XX
 PD 26-NOV-1998.
 XX
 FF 05-MAY-1998; 98W0-GB01297.
 PR 20-MAY-1997; 97GB-0010370.
 XX
 PA (ZENECA LTD.
 XX
 PI Bird CR, Medina-Suarez RDJ, Seymour GB;

Search completed: June 19, 2003, 12:46:56
 Job time : 184 secs



GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2003, 11:40:35 ; (search time 1102 seconds)

11845.338 Million cell updates/sec

Title: US-09-966-881-13

Perfect score: 806

Sequence: 1 TGTCTCTCTCTGGATCACA.....TCCCTCTCCATGGATNG 806

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB Seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST :

EST: *

1: em_leetba: *
2: em_lesthum: *
3: em_lestin: *
4: em_lestmu: *
5: em_lestov: *
6: em_lestapl: *
7: em_lestro: *
8: em_lehic: *
9: qb_est1: *
10: qb_est2: *
11: qb_htc: *
12: qb_est3: *
13: qb_est4: *
14: qb_est5: *
15: em_estom: *
16: em_estfun: *
17: qb_gss: *
18: em_gss_hum: *
19: em_gss_inv: *
20: em_gss_pnt: *
21: em_gss_vrt: *
22: em_gss_fun: *
23: em_gss_mean: *
24: em_gss_mus: *
25: em_gss_other: *
26: em_gss_pro: *
27: em_gss_rnd: *

7 165 20.5 720 14 BQ870176

8 164.4 20.4 784 17 A2916009

9 162.4 20.1 685 14 EST 49866

10 150 18.6 632 13 B1959076

11 149.4 18.5 679 10 AV822011

12 149.2 18.5 883 11 BE035831

13 144.8 18.0 612 14 BQ148154

14 143.8 17.8 420 14 BQ134100

15 141.2 17.5 518 14 BQ104182

16 141 17.5 365 12 BF655654

17 140.2 17.4 634 10 AW223193

18 139.8 17.3 789 12 BG599600

19 138.8 17.2 541 10 AW398301

20 133.8 16.6 632 14 BQ148911

21 130.4 16.5 541 10 BQ150757

22 130.2 16.2 542 12 BQ040772

23 130 16.1 629 10 AV827058

24 129.6 16.1 620 10 AV825500

25 126.6 15.7 539 10 AV527181

26 126.4 15.7 579 10 AV442702

27 126.4 15.7 727 14 BQ634030

28 125.8 15.6 362 10 AV420958

29 124.4 15.4 635 14 BQ700242

30 124.2 15.4 609 17 BH717800

31 123.6 15.3 515 14 BQ634633

32 122.4 15.2 672 13 BQ1924648

33 122.4 15.2 686 14 BQ401767

34 122.4 15.2 876 12 BQ441931

35 121.4 15.1 764 17 BH583673

36 120.4 14.9 436 12 BQ119625

37 120.2 14.9 786 17 BH647126

38 119.4 14.8 605 12 BQ045860

39 117.4 14.6 666 12 BQ592979

40 117.4 14.6 773 14 BQ508106

41 116 14.4 728 14 BQ699768

42 115.4 14.3 473 13 BQ492945

43 115 14.3 546 12 BQ008833

44 114.8 14.2 644 10 AW683073

45 114 14.1 567 13 BQ171247

ALIGNMENTS

RESULT 1 AI770665 LOCUS AI770665 DEFINITION 606055G03_x2_606 - 501 bp mRNA linear EST 02-FEB-2000

ACCESSION A1770665 KEYWORDS EST. SOURCE zea mays ORGANISM Bokaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Poaceae; PACC

REFERENCE 1 (bases 1 to 501) TITL Maize ESTs from various cDNA libraries sequenced at Stanford University

COMMENT JOURNAL Unpublished (1999) Contact: Walbot V

Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu

Plate: 606055 Row: G Column: 03. Location/Qualifiers

FEATURES Source 1/.501 /organism="zea mays"

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT NO. Score Match Length DB ID Description

1 185 23.0 501 9 A1770665

A1770665 606055G03

AJ469163 AJ469163

AZ135244 OSJNBB011

BQ741525 saq19611.

BH874844 hq82a6.b

BQ999911 QGG23G08.

source 1. -480 /organism="Hordeum vulgare"
 /db_xref="taxon:4513"
 /clone="S000800244H10F1"
 /clone_1ib="S000800244H10F1"
 /tissue_type="Callus"
 /tissue_type="Callus"
 /lab="XNLR (Stratagene)"
 /note="Organ: immature ear; Vector: pBK-CMV; Site_1: ECORI
 ; Site_2: XbaI; Mixed ear tissue cDNA library from Schmidt
 lab"
 BASE COUNT 102 a 175 c 134 g 69 t
 ORIGIN Query Match 21.8%; Score 176; DB 9; Length 480;
 Best Local Similarity 68.2%; Pred. No. 4.5e-42;
 Matches 300; Conservative 0; Mismatches 132; Indels 8; Gaps 5;
 QY 312 GGTCTGATGACCAATACTAACAGCACGGCTCGAGATCTCTGGTACTGTCGCGG 371
 Db 6 GCTCTGAGTCATCACACATCACGCCCGCGAAATCGGGTACTGTCGCGG 65
 QY 372 TTCAAGCAGAACCGATCAGAGACTCTGGGGTGGACCTGATGTCACAGAA 431
 Db 66 GACAGGCAACCCATCAGAACGACTCTGGGCTGGAGACTGGACTGTCGACAC 125
 QY 432 AAACGCTGCGTCACTGGCGATGGCTTGACGCACCCNATANGTGGCGGACGGGA 491
 Db 126 GCGCCTCGCGCAGCTGTGGCATCGCGCTTGCGCCGAAACCGCATGGCGCGTAC-GGCA 184
 QY 492 ATTTGTCCTGTTGACAGACATCCGGGAGATGATCCCGTGAATCCCTGGGAA 551
 Db 185 AGAACATACGGTGTACCCGAGGAGACCA-CTCTGTCACCCGGCAAGGGACCA 243
 QY 552 CTANATACCCGTTGCGAAGATGCGCCCTCTGGATGCCCTTAACGNCNAA 611
 Db 244 CTGGCTACGGCTCATCCAGGA---GAGCCGCTCTGATCATCTCAGGGACAT 299
 QY 612 GGAATCTCTNCTNANGGAGAACTCTNTATGACAGCTTAAACNACNATGAGACNN 671
 Db 300 GGTCTACGGCTC-AAGGGAGGTCTCATGACAGCTCAAGACCATCGACGGACGG 358
 QY 672 GTCGCCCTGTCACATGCCAATGGGCCCTGCCWICACANCCAAATTCTCCCAAC 731
 Db 359 GCGCAACTGTCACATGCCAATGGGCCCTGCCWICACANCCAAATTCTCCCAAC 417
 QY 732 TTCTCCCTGCTCCNCTCCC 753
 Db 418 ATCATCCAGGGCTCCACATCC 439
 RESULT 2
 AJ469163 LOCUS AJ469163 480 bp mRNA linear EST 24-MAY-2002
 DEFINITION Hordeum vulgare cDNA clone s000800244H10F1, mRNA
 ACCESSION AJ469163
 VERSION AJ469163.1 GI:21185119
 KEYWORDS EST.
 SOURCE
 ORGANISM Hordeum vulgare.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Hordeum.
 ; (bases 1 to 480)
 1 (bases 1 to 480)
 Saren, A.-M., Tanskanen, J., Paulin, L. and Schulman, A.H.
 COMMENT
 Unpublished (2002)
 Contact: Schulman AH
 Institute of Biotechnology
 P.O. Box 56 (Vilkinkkaari 6A), University of Helsinki FIN-00014, Finland.
 FEATURES Location/Qualifiers

source 1. -480 /organism="Hordeum vulgare"
 /db_xref="taxon:4513"
 /clone="S000800244H10F1"
 /clone_1ib="S000800244H10F1"
 /tissue_type="Callus"
 /tissue_type="Callus"
 /lab="XNLR (Stratagene)"
 /note="Organ: immature ear; Vector: pBK-CMV; Site_1: ECORI
 ; Site_2: XbaI; Mixed ear tissue cDNA library from Schmidt
 lab"
 BASE COUNT 111 a 178 c 137 g 75 t
 ORIGIN Query Match 23.0%; Score 195; DB 9; Length 501;
 Best Local Similarity 69.2%; Pred. No. 8.7e-45;
 Matches 306; Conservative 0; Mismatches 128; Indels 8; Gaps 5;
 QY 312 GGTCTGATGACCAATACTAACAGCACGGCTCGAGATCTCTGGTACTGTCGCGG 371
 Db 6 GCTCTGAGTCATCACACATCACGCCCGCGAAATCGGGTACTGTCGCGG 65
 QY 372 TTCAAGCAGAACCGATCAGAGACTCTGGGGTGGACCTGATGTCACAGAA 431
 Db 66 GACAGGCAACCCATCAGAACGACTCTGGGCTGGAGACTGGACTGTCGACAC 125
 QY 432 AAACGCTGCGTCACTGGCGATGGCTTGACGCACCCNATANGTGGCGGACGGGA 491
 Db 126 GCGCCTCGCGCAGCTGTGGCATCGCGCTTGCGCCGAAACCGCATGGCGCGTAC-GGCA 184
 QY 492 ATTTGTCCTGTTGACAGACATCCGGGAGATGATCCCGTGAATCCCTGGGAA 551
 Db 185 AGAACATACGGTGTACCCGAGGAGACCA-CTCTGTCACCCGGCAAGGGACCA 243
 QY 552 CTANATACCCGTTGCGAAGATGCGCCCTCTGGATGCCCTTAACGNCNAA 611
 Db 244 CTGGCTACGGCTCATCCAGGA---GAGCCGCTCTGATCATCTCAGGGACAT 299
 QY 612 GGAATCTCTNCTNANGGAGAACTCTNTATGACAGCTTAAACNACNATGAGACNN 671
 Db 300 GGTCTACGGCTC-AAGGGAGGTCTCATGACAGCTCAAGACCATCGACGGACGG 358
 QY 672 GTCGCCCTGTCACATGCCAATGGGCCCTGCCWICACANCCAAATTCTCCCAAC 731
 Db 359 GCGCAACTGTCACATGCCAATGGGCCCTGCCWICACANCCAAATTCTCCCAAC 417
 QY 732 TTCTCCCTGCTCCNCTCCC 753
 Db 418 ATCATCCAGGGCTCCACATCC 439
 RESULT 3
 AZI35244 LOCUS AZI35244 589 bp DNA linear GSS 02-JUN-2000
 DEFINITION OSJNB0115A18r CUGI Rice BAC library (ECORI) Oryza sativa genomic clone OSJNB0115A18r, DNA sequence.
 ACCESSION AZI35244
 VERSION AZI35244.1 GI:8214537
 KEYWORDS GSS.
 SOURCE
 ORGANISM Oryza sativa.
 REFERENCE Wing, R.A. and Dean, R.A.
 AUTHORS A BAC End Sequencing Framework to Sequence the Rice Genome
 TITLE Unpublished (1998)
 JOURNAL COMMENT Contact: Wing RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: rwing@clemson.edu
 Seq primer: GGAACAGCTATGACATG
 Class: BAC ends

FEATURES	High quality sequence start: 21 High quality sequence stop: 547.	RESULT 4
source	Location/Qualifiers	BO741525.
	1..589	BO741525.
	/organism="Oryza sativa"	saqlBell.y1 Gm-c1045 Glycine max mRNA clone SOYBEAN CLONE ID: 5
	/strain="Nipponbare"	similar to TR:024416 024416 PCTATE LYASE. ; mRNA sequence.
	/db_xref="Taxon:4530"	EST
	/clone="OSNBB0115A18r"	EST
	/clone_lid="CUGI Rice BAC Library (ECORI)"	EST
	/tissue_type="Leaf"	EST
	/lab_host="E. coli DH10B"	EST
	/note="vector: pBACIndigo; site_1: ECORI; site_2: ECORI;	EST
	Rice is the most important food crop in the world. Half of	EST
	the world population, especially those inhabiting highly	EST
	populated areas of the humid tropics and subtropics, rely	EST
	on rice as their primary source of carbohydrate.	EST
	Monocotyledonous rice is a diploid plant (2n=24) with a	EST
	haploid genome equivalent of 431 Mbp (Arunmaganathan and	EST
	Barile, 1991). The relatively small genome of rice, three	EST
	times larger than that of Arabidopsis, makes it suitable	EST
	for genomic studies. In order to facilitate positional	EST
	cloning, physical mapping and genome sequencing of rice,	EST
	we have constructed a BAC library from <i>Oryza sativa</i> .	EST
	Nipponbare variety using EcoRI as the cloning enzyme. The	EST
	library contains 55,296 clones with an average insert size	EST
	of 121 Kb providing approximately 15 haploid genome	EST
	equivalents. The deep coverage allows the isolation a	EST
	particular sequence with a probability of 99.9 %. Three	EST
	high density filters, each containing 18,432 clones	EST
	(doubly spotted), represent the whole library for colony	EST
	screening and can be requested from the Clemson University	EST
	BAC/EST Resource Center (www.genome.clemson.edu).	EST
BASE COUNT	121 a 203 c 171 g 91 t 3 others	
ORIGIN		
	Query Match 21.5% Score 173.5; DB 17; Length 589;	
	Best Local Similarity 68.1%; Pred. No. 2,7e-41; Matches 297; Conservative 0; Mismatches 131; Indels 8; Gaps 5;	
QY	314 TCTGTATGACCATATAATCACACAGCACGGCGGTCAGATCTCTGGTTATCTGTCCTGGTT 373	
DP	1 TCATCAGGTCGATCAGGAACAGACGGGAGGAGACCTGGCTTACCTGCTGCGCA 60	
QY	374 CAGCCAACCGGAGCAGCACTGCGGCTGCGACCTGGCTGATTCAGTCACAGAAAAA 433	
DP	61 CCGGCAATCCGATGACCACTGCTGGAGGCTGGACAGAACATGCCAG 120	
QY	434 AGCTGGCGTACCTGGCGATGGCTTGGACGCAACGCAATANGTGGCGGAGGGGAT 493	
DP	121 GGCTCGCGGACTCGGGCATGGGCTCGGCCAACGCCATGGGGCGGAC-GGCAG 179	
QY	494 TGTCTGGTGTGACAGACTGGGAGCATGATCCCGTGAATCTCCGGGAAACT 553	
DP	180 ATCTACGGTGTACCGGACGCCAGGACGA-CGGCTGAACTCCCGGACCT 238	
QY	554 TANATACCCCGTGTCCANGAAGTGTGCCCTCTGGATCCCTTAAACNCNAWNG 613	
DP	239 CGCGTACCGCGTATCC---GGGAGGCGGCCGCTGATCGTCTCAAGGGACATGG 294	
QY	614 AAATCTCCTCNANGGAGAAGCTNTTATGACAGCTTAACNACNATGAGTGGACNNGCT 673	
DP	295 TGAATCCTC-AAGCAGGAGCTGATCATGACAGCTTAAGACCATGACGCCGCG 353	
QY	674 GTCTCTGGCCACATGGCAATGGCCCTGCNTACCCANCAATTCTNCCAACNCTT 733	
DP	354 GCCAACGAGCACATGCCAATGGGCCATGGCCCTGCNTACCCANCAATTCTNCCAACNCTT 412	
QY	734 CTTCCTNCCCTCNC 749	
DP	413 CATCCATGGCTGC 428	
BASE COUNT	149 a 171 c 169 g 106 t	
ORIGIN		
	Query Match 21.1% Score 170; DB 14; Length 595;	
	Best Local Similarity 63.7%; Pred. No. 3..3e-40; Matches 307; Conservative 0; Mismatches 168; Indels 7; Gaps 4;	
QY	236 ATGGCTCCCTGGAGAGAGGGCTGTAACCGGGAGAACGCCACTCGACGCCCG 295	
DP	117 ATGGCTCAATGGAGAAGGTCTGGAGACTGCTGTTGAGTACATGCTGCTGATCCAG 176	
QY	296 AGGAGGATGCTGAGCTGGCTCTGATGACCATATACTAACAGCAGGCGCAGATCTCTG 355	
DP	177 AGGGATGCTCCATGGTGTGAGGACCATAGCAACTACAGGCTCGAAGGAACCTGA 236	
QY	356 GTTATCTGTCGTCGGGTCAGGCCAACCGATCGACGACTCTGGCTGGCGAACCTGATT 415	

RESULT	8	LOCUS	AZ916009	784 bp	DNA	linear	GSS 15-MAR-2001	EST 30-JUL-2002
DEFINITION	REF T1_h12-c-1_0 Maize PstI B73 Leaf	SEQUENCE	zea					
ACCESSION	AZ916009	KEYWORDS	GSS					
VERSION	AZ916009.1	JOURNAL	GI:13347280					
SOURCE	zea mays	COMMENT						
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Pancoidae; Andropogoneae; zea.	FEATURES	base 1 to 784					
REFERENCE	Missouri Maize Project-Maize Mapping Project.	SOURCE						
AUTHORS		COMMENT	Unpublished (2001)					
TITLE	PstI Zea mays B73 PstI leaf tissue library	CONTACT	Contact: Schroeder S					
JOURNAL		MISSOURI MAIZE PROJECT--MAIZE MAPPING PROJECT						
CLASS	University of Missouri	FEATURES	Location/Qualifiers					
BASE COUNT	209	SOURCE	209 Curtis Hall, Columbia, MO 65211, USA					
ORIGIN		1. .784						
FEATURES	base 1 to 655	COMMENT						
SOURCE		CONTACT	Romieu C.					
1. .784	REFERENCE	Unité de Recherche des Produits de la Vigne						
	AUTHORS	Institut National de la Recherche Agronomique						
	TITLE	2, place Viala, 34 060 Montpellier Cedex 01, France						
	JOURNAL	TEL: 00-33-(0)4-99-61-28-62						
	COMMENT	FAX: 00-33-(0)4-99-61-28-57						
		Email: romieu@ensam.inra.fr						
		Seq primer: T7.						
FEATURES	base 1 to 655	FEATURES	Location/Qualifiers					
SOURCE		1. .685						
1. .685	REFERENCE	/organism="Vitis vinifera"						
	AUTHORS	/db_xref="Shiraz"						
	TITLE	/db_xref="taxon:29760"						
	JOURNAL	/clone.lib="Ripening grape berries Lambda zap II Library"						
	COMMENT	/clone.lib="Ripening grape berries Lambda zap II Library"						
		/note="Organ: Fruit; Vector: Lambda zap II; Site:1: Eco RI						
		; site 2: XbaI; Oriented library, construction described						
		in Generation of ESTs from grape Berry (skin, pulp or						
		seeds) at various developmental stages by Terrier,N.,						
		Georges,A., Abbal,P., Romieu,C. in J. Plant Physiol. 158						
		(12): 1575-83 (2001)						
FEATURES	base 1 to 666	FEATURES	Location/Qualifiers					
SOURCE		1. .666						
1. .666	REFERENCE	/organism="Vitis vinifera"						
	AUTHORS	/db_xref="Shiraz"						
	TITLE	/db_xref="taxon:29760"						
	JOURNAL	/clone.lib="Ripening grape berries Lambda zap II Library"						
	COMMENT	/clone.lib="Ripening grape berries Lambda zap II Library"						
		/note="Organ: Fruit; Vector: Lambda zap II; Site:1: Eco RI						
		; site 2: XbaI; Oriented library, construction described						
		in Generation of ESTs from grape Berry (skin, pulp or						
		seeds) at various developmental stages by Terrier,N.,						
		Georges,A., Abbal,P., Romieu,C. in J. Plant Physiol. 158						
		(12): 1575-83 (2001)						
FEATURES	base 1 to 666	FEATURES	Location/Qualifiers					
SOURCE		1. .666						
1. .666	REFERENCE	/organism="Vitis vinifera"						
	AUTHORS	/db_xref="Shiraz"						
	TITLE	/db_xref="taxon:29760"						
	JOURNAL	/clone.lib="Ripening grape berries Lambda zap II Library"						
	COMMENT	/clone.lib="Ripening grape berries Lambda zap II Library"						
		/note="Organ: Fruit; Vector: Lambda zap II; Site:1: Eco RI						
		; site 2: XbaI; Oriented library, construction described						
		in Generation of ESTs from grape Berry (skin, pulp or						
		seeds) at various developmental stages by Terrier,N.,						
		Georges,A., Abbal,P., Romieu,C. in J. Plant Physiol. 158						
		(12): 1575-83 (2001)						
FEATURES	base 1 to 666	FEATURES	Location/Qualifiers					
SOURCE		1. .666						
1. .666	REFERENCE	/organism="Vitis vinifera"						
	AUTHORS	/db_xref="Shiraz"						
	TITLE	/db_xref="taxon:29760"						
	JOURNAL	/clone.lib="Ripening grape berries Lambda zap II Library"						
	COMMENT	/clone.lib="Ripening grape berries Lambda zap II Library"						
		/note="Organ: Fruit; Vector: Lambda zap II; Site:1: Eco RI						
		; site 2: XbaI; Oriented library, construction described						
		in Generation of ESTs from grape Berry (skin, pulp or						
		seeds) at various developmental stages by Terrier,N.,						
		Georges,A., Abbal,P., Romieu,C. in J. Plant Physiol. 158						
		(12): 1575-83 (2001)						
FEATURES	base 1 to 666	FEATURES	Location/Qualifiers					
SOURCE		1. .666						
1. .666	REFERENCE	/organism="Vitis vinifera"						
	AUTHORS	/db_xref="Shiraz"						
	TITLE	/db_xref="taxon:29760"						
	JOURNAL	/clone.lib="Ripening grape berries Lambda zap II Library"						
	COMMENT	/clone.lib="Ripening grape berries Lambda zap II Library"						
		/note="Organ: Fruit; Vector: Lambda zap II; Site:1: Eco RI						
		; site 2: XbaI; Oriented library, construction described						
		in Generation of ESTs from grape Berry (skin, pulp or						
		seeds) at various developmental stages by Terrier,N.,						
		Georges,A., Abbal,P., Romieu,C. in J. Plant Physiol. 158						
		(12): 1575-83 (2001)						
FEATURES	base 1 to 666	FEATURES	Location/Qualifiers					
SOURCE		1. .666						
1. .666	REFERENCE	/organism="Vitis vinifera"						
	AUTHORS	/db_xref="Shiraz"						
	TITLE	/db_xref="taxon:29760"						
	JOURNAL	/clone.lib="Ripening grape berries Lambda zap II Library"						
	COMMENT	/clone.lib="Ripening grape berries Lambda zap II Library"						
		/note="Organ: Fruit; Vector: Lambda zap II; Site:1: Eco RI						
		; site 2: XbaI; Oriented library, construction described						
		in Generation of ESTs from grape Berry (skin, pulp or						
		seeds) at various developmental stages by Terrier,N.,						
		Georges,A., Abbal,P., Romieu,C. in J. Plant Physiol. 158						
		(12): 1575-83 (2001)						
FEATURES	base 1 to 666	FEATURES	Location/Qualifiers					
SOURCE		1. .666						
1. .666	REFERENCE	/organism="Vitis vinifera"						
	AUTHORS	/db_xref="Shiraz"						
	TITLE	/db_xref="taxon:29760"						
	JOURNAL	/clone.lib="Ripening grape berries Lambda zap II Library"						
	COMMENT	/clone.lib="Ripening grape berries Lambda zap II Library"						
		/note="Organ: Fruit; Vector: Lambda zap II; Site:1: Eco RI						
		; site 2: XbaI; Oriented library, construction described						
		in Generation of ESTs from grape Berry (skin, pulp or						
		seeds) at various developmental stages by Terrier,N.,						
		Georges,A., Abbal,P., Romieu,C. in J. Plant Physiol. 158						
		(12): 1575-83 (2001)						
FEATURES	base 1 to 666	FEATURES	Location/Qualifiers					
SOURCE		1. .666						
1. .666	REFERENCE	/organism="Vitis vinifera"						
	AUTHORS	/db_xref="Shiraz"						
	TITLE	/db_xref="taxon:29760"						
	JOURNAL	/clone.lib="Ripening grape berries Lambda zap II Library"						
	COMMENT	/clone.lib="Ripening grape berries Lambda zap II Library"						
		/note="Organ: Fruit; Vector: Lambda zap II; Site:1: Eco RI						
		; site 2: XbaI; Oriented library, construction described						
		in Generation of ESTs from grape Berry (skin, pulp or						
		seeds) at various developmental stages by Terrier,N.,						
		Georges,A., Abbal,P., Romieu,C. in J. Plant Physiol. 158						
		(12): 1575-83 (2001)						
FEATURES	base 1 to 666	FEATURES	Location/Qualifiers					
SOURCE		1. .666						
1. .666	REFERENCE	/organism="Vitis vinifera"						
	AUTHORS	/db_xref="Shiraz"						
	TITLE	/db_xref="taxon:29760"						
	JOURNAL	/clone.lib="Ripening grape berries Lambda zap II Library"						
	COMMENT	/clone.lib="Ripening grape berries Lambda zap II Library"						
		/note="Organ: Fruit; Vector: Lambda zap II; Site:1: Eco RI						
		; site 2: XbaI; Oriented library, construction described						
		in Generation of ESTs from grape Berry (skin, pulp or						
		seeds) at various developmental stages by Terrier,N.,						
		Georges,A., Abbal,P., Romieu,C. in J. Plant Physiol. 158						
		(12): 1575-83 (2001)						
FEATURES	base 1 to 666	FEATURES	Location/Qualifiers					
SOURCE		1. .666						
1. .666	REFERENCE	/organism="Vitis vinifera"						
	AUTHORS	/db_xref="Shiraz"						
	TITLE	/db_xref="taxon:29760"						
	JOURNAL	/clone.lib="Ripening grape berries Lambda zap II Library"						
	COMMENT	/clone.lib="Ripening grape berries Lambda zap II Library"						
		/note="Organ: Fruit; Vector: Lambda zap II; Site:1: Eco RI						
		; site 2: XbaI; Oriented library, construction described						
		in Generation of ESTs from grape Berry (skin, pulp or						
		seeds) at various developmental stages by Terrier,N.,						
		Georges,A., Abbal,P., Romieu,C. in J. Plant Physiol. 158						
		(12): 1575-83 (2001)						
FEATURES	base 1 to 666	FEATURES	Location/Qualifiers					
SOURCE		1. .666						
1. .666	REFERENCE	/organism="Vitis vinifera"						
	AUTHORS	/db_xref="Shiraz"						
	TITLE	/db_xref="taxon:29760"						
	JOURNAL	/clone.lib="Ripening grape berries Lambda zap II Library"						
	COMMENT	/clone.lib="Ripening grape berries Lambda zap II Library"						
		/note="Organ: Fruit; Vector: Lambda zap II; Site:1: Eco RI						
		; site 2: XbaI; Oriented library, construction described						
		in Generation of ESTs from grape Berry (skin, pulp or						
		seeds) at various developmental stages by Terrier,N.,						
		Georges,A., Abbal,P., Romieu,C. in J. Plant Physiol. 158						
		(12): 1575-83 (2001)						
FEATURES	base 1 to 666	FEATURES	Location/Qualifiers					
SOURCE		1. .666						
1. .666	REFERENCE	/organism="Vitis vinifera"						
	AUTHORS	/db_xref="Shiraz"						
	TITLE	/db_xref="taxon:29760"						
	JOURNAL	/clone.lib="Ripening grape berries Lambda zap II Library"						
	COMMENT	/clone.lib="Ripening grape berries Lambda zap II Library"						
		/note="Organ: Fruit; Vector: Lambda zap II; Site:1: Eco RI						
		; site 2: XbaI; Oriented library, construction described						
		in Generation of ESTs from grape Berry (skin, pulp or						
		seeds) at various developmental stages by Terrier,N.,						
		Georges,A., Abbal,P., Romieu,C. in J. Plant Physiol. 158						
		(12): 1575-83 (2001)						
FEATURES	base 1 to 666	FEATURES	Location/Qualifiers					
SOURCE		1. .666						
1. .666	REFERENCE	/organism="Vitis vinifera"						
	AUTHORS	/db_xref="Shiraz"						
	TITLE	/db_xref="taxon:29760"						
	JOURNAL	/clone.lib="Ripening grape berries Lambda zap II Library"						
	COMMENT	/clone.lib="Ripening grape berries Lambda zap II Library"						
		/note="Organ: Fruit; Vector: Lambda zap II; Site:1: Eco RI						
		; site 2: XbaI; Oriented library, construction described						
		in Generation of ESTs from grape Berry (skin, pulp or						
		seeds) at various developmental stages by Terrier,N.,						
		Georges,A., Abbal,P., Romieu,C. in J. Plant Physiol. 158						
		(12): 1575-83 (2001)						
FEATURES	base 1 to 666	FEATURES	Location/Qualifiers					
SOURCE		1. .666						
1. .666	REFERENCE	/organism="Vitis vinifera"						

Db	559	CATGACACCTCTAACACATGATGGGGTGAATGCTATGGAC	618	Query Match 18.6%; Score 150; DB 13; Length 632;
Oy	700	CTGCNTTACCACTAATTCNTCCCCAACNTCTCTTCNTNGCCTCCNCTCC	752	Best local Similarity 67.2%; Pred. No. 4e-34;
Db	619	ATGCATCACCGTCAATTGTGACGAACTGTTAAATCAGGCTCACATCC	671	Matches 254; Conservative 0; Mismatches 117; Indels 7; Gaps 4;
				source
				RESULT 10
BIG59076	BIG59076	632 bp mRNA linear EST 22-OCT-2001		
LOCUS	BIG59076	(normal) Hordeum vulgare cDNA clone HVSMEN0018A17f, mRNA sequence.		
DEFINITION	BIG59076			
VERSION	BIG59076.1	GR:16310331		
KEYWORDS		EST		
SOURCE		Hordeum vulgare.		
ORGANISM		Eukaryota; Viriplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Hordeae.		
REFERENCE	1	(bases 1 to 632)		
AUTHORS	Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Chin,A., Begum,D., Frisch,D., Atkins,M., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Oates,R. and Main,D.			
TITLE		Development of a genetically and physically anchored EST resource for barley genomics: Morex rachis cDNA library		
JOURNAL		Unpublished (2001)		
COMMENT		Contact: Wing RA		
		Clemson University Genomics Institute		
		Clemson University		
		100 Jordan Hall, Clemson, SC 29634, USA		
		Tel: 864 656 7288		
		Fax: 864 656 4293		
		Email: rwng@clemson.edu		
		Total hg bases = 473		
		Seq. primer: ATTTAACCTCACTAAAGGG		
FEATURES		High quality sequence stop: 613.		
source		Location/Qualifiers		
	1.	. 632		
		/organism="Hordeum vulgare"		
		/cultivar="Morex"		
		/db_xref="taxon:4513"		
		/clone="HVSMEN0018A17f"		
		(normal)		
		/clone_1= "Hordeum vulgare rachis EST library HVCDNA0015		
		/tissue_type="Rachis"		
		/lab_host="TJCL21"		
		XhoI: Plants were grown at Washington State University, Pullman, WA in a greenhouse, the rachises were excised and frozen in liquid nitrogen (Kleinhofs lab). In the TJ Close lab at the University of California, Riverside total RNA was prepared, poly(A) was purified, one primary RNA unamplified cDNA library was made, and 1 million pfu were		
		in vivo excised to give pBluescript SK(-) cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see		
		http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/lgn/31/cover.html)"		
FEATURES		FEATURES		
source		source		
	1.	. 679		
		/organism="Arabidopsis thaliana"		
		/db_xref="taxon:3702"		
		/clone="RAFL04-19-N09"		
		/clone_1= "RAFL4"		
		/dev_stage="rosette plants"		

BASE COUNT		217 a	201 c.	221 g	241 t	3 others
<i>/note="Site-1: SstI; Site-2: XbaI; subjected to cold-treated(1,2,5,10,24 hr)"</i>						
ORIGIN						
<i>/lab host="SOLR"</i>						
BASE COUNT	184	a	182	c	137	g
FEATURES						
source	1. . 883	<i>/organism="Mesembryanthemum crystallinum"</i>				
		<i>/db_xref="taxon:3544"</i>				
		<i>/clone_lib="MO"</i>				
		<i>/tissue_type="apical meristem and leaf primordia"</i>				
		<i>/dev_stage="5 weeks"</i>				
FEATURES						
source	1. . 612	<i>/Location/Qualifiers</i>				
RESULT	12					
BE035831						
LOCUS	BE035831					
DEFINITION	MO10G11 MO Mesembryanthemum crystallinum cDNA 5' similar to pectate lyase, mRNA sequence.					
ACCESSION	BE035831.1					
VERSION	GI:8330840					
KEYWORDS						
SOURCE						
ORGANISM	Mesembryanthemum crystallinum					
	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Alzoaceae; Mesembryanthemum. (bases 1 to 883)					
REFERENCE	Bohnet, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M., Ferrea, H., Kawasaki, S., McCollough, A., Michalowski, C.B., Palacio-C., Scar, G., Wheeler, M. and Zepeda, G.R.					
AUTHORS	Functional Genomics of Plant Stress Tolerance					
JOURNAL	Unpublished (2000)					
COMMENT	Contact: Michalowski, C.B.					
Bio Sciences West room 513, Tucson, AZ 85721, USA						
Tel: 520-621-1982						
Fax: 520-621-1697						
Email: cbm@u.arizona.edu						
An open reading frame exists.						
Insert Length: 2 Std Error: 0.00.						
Location/Qualifiers						
RESULT	13					
BE048154						
LOCUS	BE048154					
DEFINITION	NE062C07FL1054 Developing flower Medicago truncatula cDNA clone					
ACCESSION	NE062C07FL 5'					
VERSION	GI:148154					
KEYWORDS						
SOURCE						
ORGANISM	Medicago truncatula					
	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Fabales; Papilionoideae; Trifolieae; Medicago. (bases 1 to 612)					
REFERENCE	Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Iman, J.T., Weller, J.W. and May, G.D.					
AUTHORS	Expressed Sequence Tags from the Samuel Roberts Noble Foundation					
JOURNAL	Medicago truncatula flower library					
COMMENT	Unpublished (2001)					
	Contact: May, G.D.					
	Plant Biology Division					
	The Samuel Roberts Noble Foundation					
	2510 Sam Noble Parkway, Ardmore, OK 73402, USA					
	Tel: 580 221 7391					
	Fax: 580 221 7380					
	Email: gdmay@noble.org					
FEATURES						
source	1. . 612					
	Insert Length: 612 Std Error: 0.00					
	Plate: 062 row: C column: 07					
	Seq primer: TCCACAGAAAGAGCTATGAC					
	Location/Qualifiers					

				ORGANISM	Glycine max
				Eukarya; Viriplantae; Streptophyta; Embryophyta; Tracheophyta;	
				Spermatophyta; Magnoliophyta; eudicots; core eudicots;	
				Rosidae; eurosids I; Fabales; Papilioideae; Phaseoleae;	
				Glycine.	
				1 (bases 1 to 420)	
				Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Stepcik, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.	
				Public Soybean EST Project	
				Unpublished (1999)	
				Contact: Shoemaker R/Public soybean EST Project	
				Public Soybean EST Project	
				Washington University School of Medicine	
				444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA	
				Tel: 314-286-1800	
				Fax: 314-286-1810	
				Email: est@wustl.edu	
				This clone is available through: ResGen, Invitrogen Corp, 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact: oucresgen.com web site: www.resgen.com	
				Seq. primer: -40RP from Gibco.	
				1. 420	
				FEATURES	
				SOURCE	
Qy	246	GGAAGAGAGGGCTGTAACCGGGCAGCAGGCGAGTCGACGACCCGGAGGTTGC	305		
Db	25	GGAAACACAGCTGAGAAATGATGAGCGCTCTGGCTTAATCCAAAGAGGGCG	84		
Qy	306	TTGACCGCTCTGATGACATRATCAACAGCACGGCTCGCAGATCTCTGGTATCTGTC	365		
Db	85	TTCATGGTGGATGACATCGACATCCAGAAAGTACTGAAAGGAATCTGGATTTC	144		
Qy	366	GTGGGTCTAGGGACACCGATGACGAGCTGCTGGCGTGACCCCTGATGGCATGCTAA	425		
Db	145	GTGTGGACCGTAACTATGGACATGGTGGCGCTGACCGAACTGGCAACGCA	204		
Qy	426	CAGAAAGCTGCGTCACTGGCAGTGGCTGGACACGCNATANSTGGCGCGA	485		
Db	205	CAGGAAGGTCTAGCAGCTGCTGGTATGGTTCGGTAGAACACGCCATTGGTGGCGGA	264		
Qy	486	CGGGGAATTGGTGGCGAGACTCGGGGACNATGATGCCGCTGAGTCCCG	545		
Db	265	-TGGAAAGTACTATGTTGCTGACTGACAGATGATGATGACCA-CCCTGTTAACCTAGGCCA	322		
Qy	546	GGACACTANATACCCGTCNTCCAAAGAAGTGGCCCTCTGGATCCCTTAACN	605		
Db	323	GGAACCTTGCGCACCGGTATCCAAAGATG-----ACCACTTGGATGTCGTCAGA	377		
Qy	606	CNAANTGGAAATCTCNCTCNANGGAAGACTNTTAACTACNATCGATG	665		
Db	378	GAGACATGTTATCAGTTAACAAAGCTTATGGAACAGTTCAAGAACATTGATG	437		
				BASE COUNT	
				112 a, 88 c	
				ORIGIN	
				SOYBEAN	
				Query Match	
				17.8%; Score 143.8;	
				Best Local Similarity 63.2%; Pred. No. 2.4e-32;	
				Matches 270; Conservative 0; Mismatches 150; Indels 7; Gaps 4;	
				BASE COUNT	
				112 a, 88 c	
				ORIGIN	
				SOYBEAN	
RESULT 14				Query Match	
BQ134100				17.8%; Score 143.8;	
LCCLUS				Best Local Similarity 63.2%; Pred. No. 2.4e-32;	
				Matches 270; Conservative 0; Mismatches 150; Indels 7; Gaps 4;	
				BASE COUNT	
				112 a, 88 c	
				ORIGIN	
				SOYBEAN	
DEFINITION				Query Match	
				17.8%; Score 143.8;	
				Best Local Similarity 63.2%; Pred. No. 2.4e-32;	
				Matches 270; Conservative 0; Mismatches 150; Indels 7; Gaps 4;	
				BASE COUNT	
				112 a, 88 c	
				ORIGIN	
				SOYBEAN	
ACCESSION				Query Match	
BQ134100				17.8%; Score 143.8;	
VERSTON				Best Local Similarity 63.2%; Pred. No. 2.4e-32;	
KEYWORDS				Matches 270; Conservative 0; Mismatches 150; Indels 7; Gaps 4;	
SOURCE				BASE COUNT	
				112 a, 88 c	
				ORIGIN	
				SOYBEAN	

Qy	531 GTGATCCTGCCGGAAACATANATACCCCCTCNTCAANGAAGTGGCCCTCTG	590	Db	219 TGCAGAGATGACCCACATGGAGGCCACCGCAAGGGCTAGCCACTGGCATT	278
Db	239 GTGACCCGAAACCGGCACCTCTGCAATGCGTGATC---AGGATAAGCCATG	294	Qy	454 GGCTTGGGCAAGGCNATANGGCCGAGGGATTGTTGTTGTTGAGACTC	513
Qy	591 GATCCCTTAACNCNAANTGAAATCTCNCNANCAGAGACTCNNTATGACACCT	650	Db	279 GGTTTGGGCCAGCTCTGGCCCTGACGAGTACGTCATGATGACCT	337
Db	295 GATGTCAGAGGGACATGGTAT-TCAGCTGAAACAGAGCTGATCATGACAGCT	353	Qy	514 CGGGACNATGATCCCGTGAATCTCGCCGGAACTANATACCCGTCNTCCAN	573
Qy	651 TAAACACTGAGAGCAGNCNGTGTCTGTCACATGGCCATGGCCCTGNTCACCA	710	Db	338 CGGTCATGATGA-CCCGGTAACCCCGCCGGTACCCCTCCCTACCGTGTATCCAGG	396
Db	354 TCAGACAGATGATGGAGGACTCAATGTCATGGACATGCTAATGGACCATGATCACAA	413	Qy	574 GAAGTGCCTCTGGGACCCCTTAACNCNAANTGAAATCTCNCTNANCAGAAGA	633
Qy	711 NCCAATT 717		Db	397 ACAG---GCCTTGTGGATGTCATGGTCACATGGTGTCA-TTGAGCAGGA	451
Db	414 TTCAAGTT 420		Qy	634 ACTNTTATGAAAGCTTAAACNATGATGTCACNCNGTGTCTGTCACATGGCAA	693
			Db	452 GCTTATAAGACGCTCAAGACCATGACCTGAGTCATGGCACATGCTTA	511
			Qy	694 TGGG 698	
			Db	512 TGGAG 516	
				Search completed: June 19, 2003, 13:05:37	
				Job time : 1107 secs	
RESULT 15					
LOCUS	BO104182	518 bp mRNA linear EST 16-APR-2002			
DEFINITION	fc2443.e Rose Petals (Fragrant Cloud) Lambda Zap Express Library				
AUTHORS	Rosa hybrid cultivar cDNA clone fc2443.e 5', mRNA sequence.				
ACCESSION	BO104182				
VERSION	BO104182.1				
KEYWORDS	EST.				
TITLE	Rosa petal genomics: an integrated approach to discover fragrance related genes				
SOURCE	Rosa hybrid cultivar				
ORGANISM	Bulkytaria; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Eudicotyledons; core eudicots; Rosidae; eurosids I; Rosales; Rosaceae; Rosoideae; Rosa.				
REFERENCE	1 (bases 1 to 518)				
	Menda, N., Guterman, I., Piestun, D., Emanuel, M., Adam, Z., Pichersky, E., Lewinsohn, E., Zamir, D., Vainstein, A. and Weiss, D.				
FEATURES	petal genomics				
source	petal genomics				
COMMENT	Faculty of Agricultural, Food and Environmental Quality Sciences, The Hebrew University of Jerusalem, P.O. Box 12, Rehovot, 76100, Israel				
	Tel: 972 8 9489 389				
	Fax: 972 8 9468 263				
	Email: shaham@ri.huji.ac.il				
FEATURES	Seq primer: T3 forward.				
source	Location/qualifiers				
	1. .518				
	/organism="Rosa hybrid cultivar"				
	/strain="Fragrant Cloud"				
	/db_xref="taxon:128735"				
	/clone="fc2443.e"				
	/clone_id="Rose petals (Fragrant Cloud) Lambda Zap Express Library"				
	/tissue_type="petals"				
	/dev_stage="Young open flower at stage four"				
	/note="Vector: pBKCMV; Site_1: EcoRI; Site_2: XbaI"				
BASE COUNT	134 a 129 c 147 g 108 t				
ORIGIN					
	Qy Best Local Similarity 63.1%; Score 141.2; DB 14; Length 518; Matches 268; Conservative 0; Mismatches 150; Indels 7; Caps 4;				
Qy	274 GAAGCCGAGTCGACGACCCGAGGAGTGTGCTGAGCTCTGATCAAC 333				
Db	99 GAGCACGAGTATGATTCGGAGGAGTCGGCTTCAGGACCCGATCAGAC 158				
Qy	334 AGCACGGCTCGAGATCTTGTATCTGCTGCTGCTGAGCTAATCAAC 393				
Db	159 AGTACTGGAGAGAACTGGATTCTCTGGCAACAGGGATCCATTGATGAC 218				
Qy	394 TCTGGGGTGGGACCCCTGATGGCATGCAACAGAAAAAGCTCGCTGACTGGCAT 453				

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2003, 12:43:50 ; Search time 46 Seconds
(without alignments)
5373.510 Million cell updates/sec

Title: US-09-966-881-13
Perfect score: 806
Sequence: 1 TGTTCCTCTCCATCGACACA.....TCCCCCTCTCCTATAGGATNG 806

Scoring table: IDENTITY_NUC
gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

1: /egn2_6_ptodata/1/ina5A_COMBO.seq: *
2: /egn2_6_ptodata/1/ina6B_COMBO.seq: *
3: /egn2_6_ptodata/1/ina6B_COMBO.seq: *
4: /egn2_6_ptodata/1/ina6B_COMBO.seq: *
5: /egn2_6_ptodata/1/ina6B_COMBO.seq: *
6: /egn2_6_ptodata/1/ina6B_COMBO.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	55.6	6.9	1170	3	US-08-467-023-94		Sequence 94, Appl
2	55.2	6.8	1337	3	US-08-467-023-1		Sequence 1, Appl
3	54	6.7	1278	3	US-08-467-023-96		Sequence 96, Appl
4	46.6	5.8	1328	1	US-08-290-448A-58		Sequence 58, Appl
5	46.6	5.8	1328	1	US-08-290-448A-58		Sequence 58, Appl
6	46.6	5.8	1328	1	US-08-175-069A-58		Sequence 58, Appl
7	46.6	5.8	1328	4	US-08-461-939B-58		Sequence 58, Appl
8	46.6	5.8	1328	4	US-08-461-939B-58		Sequence 58, Appl
9	46.6	5.8	1349	1	US-08-290-448A-73		Sequence 73, Appl
10	46.6	5.8	1349	1	US-08-290-448A-73		Sequence 73, Appl
11	45.6	5.8	1349	1	US-08-069A-73		Sequence 73, Appl
12	45.6	5.8	1349	4	US-08-461-939B-73		Sequence 73, Appl
13	45.6	5.8	1349	4	US-08-461-939B-73		Sequence 73, Appl
14	46	5.7	7218	1	US-08-231-463-14		Sequence 14, Appl
15	43.8	5.4	1320	1	US-08-290-448A-75		Sequence 75, Appl
16	43.8	5.4	1320	1	US-08-290-448A-75		Sequence 75, Appl
17	43.8	5.4	1320	1	US-08-069A-75		Sequence 75, Appl
18	43.8	5.4	1320	4	US-08-461-939B-75		Sequence 75, Appl
19	43.8	5.4	1320	4	US-08-461-939B-75		Sequence 75, Appl
20	41.8	5.2	1160	1	US-08-290-448A-77		Sequence 77, Appl
21	41.8	5.2	1160	1	US-08-290-448A-77		Sequence 77, Appl
22	41.8	5.2	1160	1	US-08-175-069A-77		Sequence 77, Appl
23	41.8	5.2	1160	4	US-08-461-939B-77		Sequence 77, Appl
24	41.8	5.2	1160	4	US-08-461-939B-77		Sequence 77, Appl
25	43.8	4.8	1196	1	US-08-290-448A-71		Sequence 71, Appl
26	43.8	4.8	1196	1	US-08-290-448A-71		Sequence 71, Appl
27	4.8	1196	1	US-08-175-069A-71		Sequence 71, Appl	

INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 1170 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

RESULT 1
US 08-467-023-94
Sequence 94, Application US/08467023
; Patent No. 6090386
GENERAL INFORMATION:
APPLICANT: Griffith, Irwin J.;
APPLICANT: Pollock, Julian F.;
APPLICANT: Bond, Julian F.;
APPLICANT: Garman, Richard D.;
APPLICANT: Kuo, Mei-Chang;
APPLICANT: Weung, Siu-mei H.;
APPLICANT: Brauer, Andrew;
APPLICANT: Exley, Mark A.;
APPLICANT: Powers, Steven P.;
TITLE OF INVENTION: Allergenic Proteins And Peptides From
TITLE OF INVENTION: Japanese Cedar Pollen
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunologic Pharmaceutical Corporation, Inc.
STREET: 610 Lincoln St
CITY: Waltham
STATE: MA
COUNTRY: USA
ZIP: 02154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08467-023

FILING DATE: June 6, 1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/350,225

FILING DATE: December 6, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Jane E. Remillard

REGISTRATION NUMBER: 38,872

REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-5940

TELEFAX: (617) 227-5941

SEQUENCE 71, Appl

FEATURE:
 NAME/KEY: CDS
 LOCATION: 26..1126
 FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: 89..1126
 US-08-467-023-94

Query Match 6.9%; Score 55.6; DB 3; Length 1170;
 Best Local Similarity 62.5%; Pred. No. 2.7e-07; Mismatches 0;
 Matches 85; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 360 TCTGTCGTCTGGTCAGGCACCCGATCAGACTGCTGCTGGCTGGCAGACCTGTGATGCCA 419
 Db 73 TGTAACTTGTACTCTGATGATTCATCGACAGCTGCTGAGGAGATTCGAATGGGA 132

QY 420 TGTCAACAGAAAAGCTGCTGACTGCGGATGGCTGAGCTGGATTTGGAAGCTCCACCATGGAGG 479
 Db 133 TCAAAACAGAATGAACTGCTGAGACTGTGCTGAGGATTTGGAAGCTCCACCATGGAGG 192

QY 480 CGCGCACGGGAATT 495
 Db 193 CAAGGAGGAGATTT 208

RESULT 2
 US-08-467-023-1

Sequence 1, Application US/08467023
 ; Patent No. 6090386
 ; GENERAL INFORMATION:
 ; APPLICANT: Griffeth, Irwin J.;
 ; APPLICANT: Pollock, Joanne;
 ; APPLICANT: Bond, Julian F.;
 ; APPLICANT: Garman, Richard D;
 ; APPLICANT: Kuo, Mei-Chang;
 ; APPLICANT: Yeung, Siu-mei H.;
 ; APPLICANT: Exley, Mark A.;
 ; APPLICANT: Powers, Steven P.
 ; TITLE OF INVENTION: Allergenic Proteins And Peptides From
 ; NUMBER OF SEQUENCES: 261
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Immunologic Pharmaceutical Corporation, Inc.
 ; STREET: 610 Lincoln St
 ; CITY: Waltham
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02154
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/467, 023
 ; FILING DATE: June 6, 1995
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/355,0225
 ; FILING DATE: December 6, 1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jane E. Remillard
 ; REGISTRATION NUMBER: 38,872
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 227-7400
 ; TELEFAX: (617) 227-5941
 ; INFORMATION FOR SEQ ID NO: 1:
 ; LENGTH: 1337 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single

Query Match 6.8%; Score 55.2; DB 3; Length 1337;
 Best Local Similarity 51.7%; Pred. No. 3.8e-07; Mismatches 0;
 Matches 181; Conservative 0; Mismatches 159; Indels 10; Gaps 3;

QY 349 TCTCTGGTATCTGCTGCGGGTCAGGAACCCGATGACGAGCTGCTGCTGGCTGGTGCAC 408
 Db 102 TCTTGTGTAATTGGTCTTCTGTAATCCATAGACAGACTGCTGCTGACTGGCGCATGGCTGGAGGAGAC 161

QY 409 CCTGATGGCATGTCACAGAAAAGCTGCTGACTGCTGCTGACTGGCGCATGGCTGGAGGAGAC 468
 Db 162 TCAAACGGCCAAATAGATGAGCTGGCTGGCAGATGTCAGGGCTCGGAAGCTC 221

QY 469 GCNATANGTGCCGGACGGGAATTGTCAGTCAGACAGACCCGGACACATGATGCCA 528
 Db 222 ACCATGGGAGGCAAGGGAGGAG-ATCTTATACGGTCACGAGATGACCA---CC 276

QY 529 CCGTCATCTGCAACAGGACTCTGCGGACTANATACCCGTCNCCAAANGAAGTGCCCT 588
 Db 277 CTGTCATCTGCAACAGGACTCTGCGGACTATGAGCAACCCGGATAGCCCTGTGGA 336

QY 589 GGGATCCCTTAACACNCAANTGGAAATCTCNCTCNANGAAGAACCTNTTATGACAG 648
 Db 337 TAATTTCACTGGGATATGATATAAGCTCAAATGCCTATGTCAC---ATTCTCG 391

QY 649 CTTTANACNATGATGGACNCNGTCCCTGGTCCACATGCCATGGCG 698
 Db 392 GTATAGACTTTGATGGCAGGGAGCACAGTTATATGGCATGGCG 441

RESULT 3
 US-08-467-023-96

Sequence 95, Application US/08467023
 ; Patent No. 6090386
 ; GENERAL INFORMATION:
 ; APPLICANT: Griffeth, Irwin J.;
 ; APPLICANT: Pollock, Joanne;
 ; APPLICANT: Bond, Julian F.;
 ; APPLICANT: Garman, Richard D;
 ; APPLICANT: Kuo, Mei-Chang;
 ; APPLICANT: Yeung, Siu-mei H.;
 ; APPLICANT: Exley, Mark A.;
 ; APPLICANT: Powers, Steven P.
 ; TITLE OF INVENTION: Allergenic Proteins And Peptides From
 ; TITLE OF INVENTION: Japanese Cedar Pollen
 ; NUMBER OF SEQUENCES: 261
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Immunologic Pharmaceutical Corporation, Inc.
 ; STREET: 610 Lincoln St
 ; CITY: Waltham
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02154
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/467, 023
 ; FILING DATE: June 6, 1995

CLASSIFICATION: 424
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/3350-225
 FILING DATE: December 6, 1994

ATTORNEY/AGENT INFORMATION:
 NAME: Jane E. Remillard
 REGISTRATION NUMBER: 38,872
 REFERENCE/DOCKET NUMBER: IMI-028CPD2

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 96:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1278 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 MOLECULE TYPE: linear
 FEATURE: CDS
 NAME/KEY: CDS
 LOCATION: 36..1145
 NAME/KEY: mat_peptide
 LOCATION: 99..1145

US-08-467-023-96
 Query Match 6.7%; Score 54; DB 3; Length 1278;
 Best Local Similarity 61.8%; Pred. No. 8.6e-07; Mismatches 0; Indels 0; Gaps 0;

Matches 84; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
 Qy 360 TCTGCTGCGGTTCAGGCCAACCGATGCCGACTGCTGGCGTGCACCCGTGATGCCA 419
 Db 83 TGTATCTGTGCTGCTGATTAATCCCTAGACAGCTGCTGGAGAGGATTCGAACTGGG 142

Qy 420 TGTCAAGAAGAAAGCTCGCTGACTGGGCAATGGCTTGACGCACGCNATANSTGG 479
 Db 143 TCAAACAGAATGCAAGCTCGAGATGGCGTGGGATTGGAAAGCTCCACCATGGGG 202
 Qy 480 CGCGGACGGGAATT 495

Db 203 CAAAGGAGGAGATT 218
 US-08-290-448A-58
 Query Match 5.8%; Score 46.6; DB 1; Length 1328;
 Best Local Similarity 46.7%; Pred. No. 0.00016; Mismatches 0; Indels 7; Gaps 1;

Matches 156; Conservative 0; Mismatches 171; Indels 7; Gaps 1;
 Qy 365 CGTCGGGTTTCAGGCCAACCGATGCCGACTGCTGGCGTGCACCCGTGATGCCA 424
 Db 113 CATGGAAAGCACACAACTTATAGACAGTGCCTGGAGGTGCAAGGGATTCGGGAATA 172
 Qy 425 ACAGAAAGAGCTGCTGACTCGGCAATGGCTTGGAAGCAGCNAATANGTGCGCG 484
 Db 173 ACCGACACAGCGTAGGCCGATGGCCAGGTITGCAAGGGACCTACGGGIGAAGAAC 232

Qy 485 ACGGGAATTGGTGTGTGTGAGAGACTCCGGGACNATGATGCCCGTGAATCCTCGCC 544
 Db 233 ATGGTAT-----GTCATACAGCGTACCGAGTATAAGATGTGATGTTGCAAACTCCA 285
 Qy 545 GGGACACTTANATACCCGTCNCCCAAGAAGCTGCCCCCTGTGGATCCCTTAAC 604
 Db 286 AAAGAAGGCACACTCCGGTTGCTGCCAAACAGCCGTTGTGATCAATTAAA 345

Qy 605 NCNANTGAAATCTCNCCTNANGGAAGAACNTNTATGAAACAGCTTAANACNCGAT 664
 Db 346 AGAATATGGTGTGATCATTGACATCAAGAGCTGTCGTAACAGCGACAAGCCATCGAT 405

US-08-290-448A-58
 Sequence 58, Application US/08290448A

Patent No. 5691204

GENERAL INFORMATION:
 APPLICANT: Rogers, Bruce
 APPLICANT: Klapfer, David G.

APPLICANT: Rafnar, Thorunn

APPLICANT: Kuo, Mei-chang

TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses

NUMBER OF SEQUENCES: 93

CORRESPONDENCE ADDRESS:

ADDRESSEE: LARIVE & COCKFIELD
 STREET: 60 State Street, suite 510
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/290,448A

FILING DATE: August 15, 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/529,951

FILING DATE: May 29, 1990

APPLICATION NUMBER: US 07/325,365

FILING DATE: March 17, 1989
 ATTORNEY/AGENT INFORMATION:
 NAME: Amy E. Mandragouras
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: IMI-018CN

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 58:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1328 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 MOLECULE TYPE: linear
 FEATURE: CDS
 NAME/KEY: CDS
 LOCATION: 1..1328

US-08-290-448A-58
 Query Match 5.8%; Score 46.6; DB 1; Length 1328;
 Best Local Similarity 46.7%; Pred. No. 0.00016; Mismatches 0; Indels 7; Gaps 1;

Matches 156; Conservative 0; Mismatches 171; Indels 7; Gaps 1;
 Qy 365 CGTCGGGTTTCAGGCCAACCGATGCCGACTGCTGGCGTGCACCCGTGATGCCA 424
 Db 113 CATGGAAAGCACACAACTTATAGACAGTGCCTGGAGGTGCAAGGGATTCGGGAATA 172
 Qy 425 ACAGAAAGAGCTGCTGACTCGGCAATGGCTTGGAAGCAGCNAATANGTGCGCG 484
 Db 173 ACCGACACAGCGTAGGCCGATGGCCAGGTITGCAAGGGACCTACGGGIGAAGAAC 232

Qy 485 ACGGGAATTGGTGTGTGTGAGAGACTCCGGGACNATGATGCCCGTGAATCCTCGCC 544
 Db 233 ATGGTAT-----GTCATACAGCGTACCGAGTATAAGATGTGATGTTGCAAACTCCA 285

Qy 545 GGGACACTTANATACCCGTCNCCCAAGAAGCTGCCCCCTGTGGATCCCTTAAC 604
 Db 286 AAAGAAGGCACACTCCGGTTGCTGCCAAACAGCCGTTGTGATCAATTAAA 345

Qy 605 NCNANTGAAATCTCNCCTNANGGAAGAACNTNTATGAAACAGCTTAANACNCGAT 664
 Db 346 AGAATATGGTGTGATCATTGACATCAAGAGCTGTCGTAACAGCGACAAGCCATCGAT 405

US-08-290-448A-58
 Sequence 58, Application US/08290448A

Patent No. 5691204

GENERAL INFORMATION:
 APPLICANT: Rogers, Bruce
 APPLICANT: Klapfer, David G.

APPLICANT: Rafnar, Thorunn

APPLICANT: Kuo, Mei-chang

TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses

NUMBER OF SEQUENCES: 93

CORRESPONDENCE ADDRESS:

ADDRESSEE: LARIVE & COCKFIELD
 STREET: 60 State Street, suite 510
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US-08/290,448A
FILING DATE: August 15, 1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/529, 951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/325, 365
FILING DATE: March 17, 1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragoras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-018CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
TELEMAIL:
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 1328 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1328
US-08-290-448A-58

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, v
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/175,069
FILING DATE: December 29, 1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/529,951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: March 17, 1989
ATTORNEY / AGENT INFORMATION:
NAME: Amy E. Mandragoras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMT-018DW
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 1328 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

QY·
 Best Local Similarity 46.7%; Pred. 0; 0.0016; Mismatches 171; Indels 7; Gaps 1;
 Matches 156; Conservative 0;
 Score 5.08; DB 1; Length 1328;

QY·	365	CCTGGCGGTCAAGCACCCGATGCGACTGGGCACTGGCTTGACCCAAACGNATANGGGCG 424
Db	113	CATGTGAGCACACATATTAGACAGTGCAGGGTCAAGCCGATGGCGATA 172
QY	425	ACGAAAGAACCTGCGTGTGACTGGGCACTGGCTTGACCCAAACGNATANGGGCG 484
Db	173	ACCGACAGCGTTAGCGGATGCGCAAGGGTCAAGGACRACCGTACGGGAAAC 232
QY	485	ACGGGGATTGTGCGTGTGACAGACTCCGGGACNATGATCCCGTQAATCTCGGCC 544
Db	233	ATGGTGTAT-----GTCACGGTCAACAGTGTGCAATCC 285
QY	545	GGGAACTTANATACCCCGTCTCAANGAACGTTGCACCCCTGTGGATCCCTTAAC 604
Db	286	AAAGAAGGCACACTCCGGTTGCTGCCAAACAGGCCCTGTGGATCATTTAA 345
QY	605	NCNAAATGGAATCTCTCNCNTCNANGGAGAACNTNTATGAAACGCTTAANACNTGAT 664
Db	346	AGAAATATGGTGTATTCATGTGAACTCAGACTGCTGGTGTGAAACAGCAGCTGCGAACAGCAGCATCGAT 405
QY·	665	GGACNCNGTGTCTCGCACATGCCATGGCC 698
Db	406	GGCCGAGGGTGAAGATTAACATCGTTAACGCCG 439

RESULT 6
 US-08-175-069A-58
 Sequence 58, Application US/08175069A
 ; Patent No. 5776761
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Rogers, Bruce
 ; APPLICANT: Kipper, David G.
 ; APPLICANT: Rafnar, Thorunn
 ; APPLICANT: Kuo, Mei-chang
 ; TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
 ; NUMBER OF SEQUENCES: 93
 ;
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSE: LAHIVE & COCKFIELD, LLP
 ; STREET: 60 State Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109-1875

RESULT 11
US-08-175-069A-73
Sequence 73, Application US/08175069A
; Patent No. 5776761
; GENERAL INFORMATION:
; APPLICANT: Rogers, Bruce
; APPLICANT: Klapper, David G.
; APPLICANT: Rafaar, Thorunn
; APPLICANT: Kuo, Mei-chang
; TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patientin Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/175,069A
; FILING DATE: December 29, 1993
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/529,951
; FILING DATE: May 29, 1990
; APPLICATION NUMBER: US 07/325,365
; FILING DATE: March 17, 1989
; ATTORNEY / AGENT INFORMATION:
; NAME: Amy E. Mandragoras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-018DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1349 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1323
; ;
; US-08-175-069A-73

RESULT 12
US-08-461-939B-73
Sequence 73, Application US/08461939B
; Patent No. 6335019
; GENERAL INFORMATION:
; APPLICANT: Rogers, Bruce
; APPLICANT: Klapper, David G.
; APPLICANT: Rafaar, Thorunn
; APPLICANT: Kuo, Mei-chang
; TITLE OF INVENTION: Methods For Treating Sensitivity To A
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patientin Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,939B
; FILING DATE:
; APPLICATION NUMBER: US/08/464,000
; FILING DATE: 05 JUN 1995
; APPLICATION NUMBER: US 08/290,448
; FILING DATE: 15-AUG-1994
; APPLICATION NUMBER: US 07/529,951
; FILING DATE: 29-MAY-1990
; APPLICATION NUMBER: US 07/325,365
; FILING DATE: 17-MAR-1989
; ATTORNEY / AGENT INFORMATION:
; NAME: Amy E. Mandragoras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-018CNDV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1349 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

Query Match 5.8%; Score 46.6; DB 1; Length 1349;
Best Local Similarity 46.7%; Pred. No. 0.00016; Matches 156; Conservative 0; Mismatches 171; Indels 7; Gaps 1;
Matches 156; Conservative 0; Mismatches 171; Indels 7; Gaps 1;

TOPOLogy: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..1123
 US-08-461-938B-73

Query Match 5.8%; Score 46 6; DB 4; Length 1349;
 Best Local Similarity 46.7%; Pred. No. 0.00016; Mismatches 171; Indels 7; Gaps 1;
 Matches 156; Conservative 0; Mismatches 171; Indels 7; Gaps 1;

QY 365 CGGGGGTTCAGGAAACCGGATCGACGAGCTGCTGCGGGTGCACGGGACCTAGGGATGTCGA 424
 134 CATGTGAAACACAACTATAGACAGACAGTGCTGGAGGGCAANGCGATTGGCGA 193

QY 425 ACAGAAAAAGCTGCTGACTGCGCATGCGTGGCTTGGAGGCAACGCNATANGTGCCCG 484
 194 ACCGACAAAGCGTGTGGATGCAAAAGGGACCTAGGGATGTCGA 253

QY 485 ACGGGAATTGTTGTTGACAGACTCGGGACNATGGATCCCGTGTGGCGCC 544
 254 ATGGTGTAT-----GTCTACACGGTACACAGTGTGAAATGCAATGCCA 306

QY 545 GGGACACTANATAACCCGTCNCTCAANGAAGTGTGCCCTCTGGATCCCTTAAC 604
 307 AAAGAAGGACACTCCGGTTGCGCTGCCAACAGGCCCTGGGATTTAA 366

QY 605 NCNAANTGAAATCTCNCNCNANGAAGAAGACTCNNTATGACAGCTTANANATCCAT 664
 367 AGAATATGTTGATCATTGAACTCAAGGCTGTGCTGTAACACGGAGACATCGAT 426

Db 665 GGACNCNGTGTCCCTGTCACATGCCAATGGGG 698
 427 GGCGGAGGGTGAAGTTACATCGTTAACGCCG 460

RESULT 13
 US-08-464-000-73
 Sequence 73, Application US/08464000
 ; GENERAL INFORMATION:
 ; APPLICANT: Rogers, Bruce
 ; APPLICANT: Klapper, David G.
 ; APPLICANT: Kuo, Mei-Chang
 ; APPLICANT: Rafnar, Thorunn
 ; APPLICANT: Teng, Ming
 ; TITLE OF INVENTION: Allergenic Peptides from Ragweed Pollen
 ; NUMBER OF SEQUENCES: 93
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP
 ; STREET: 60 State Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109-1875
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/464,000
 ; FILING DATE: 05-JUN-1995
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/290,448
 ; FILING DATE: 15-AUG-1994
 ; APPLICATION NUMBER: US 07/529,951
 ; FILING DATE: 29-MAY-1990
 ; APPLICATION NUMBER: US 07/325,365
 ; FILING DATE: 17-MAR-1989
 ; ATTORNEY / AGENT INFORMATION:
 ; NAME: Amy E. Mandragoras
 ; REGISTRATION NUMBER: 36,207
 ; REFERENCE/DOCKET NUMBER: IMI-018CN2

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEFAX: (617)227-5941
 INFORMATION FOR SEO ID NO: 73:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1349 base pairs
 NAME/KEY: CDS
 LOCATION: 1..1123
 US-08-464-000-73

Query Match 5.8%; Score 46 6; DB 4; Length 1349;
 Best Local Similarity 46.7%; Pred. No. 0.00016; Mismatches 171; Indels 7; Gaps 1;
 Matches 156; Conservative 0; Mismatches 171; Indels 7; Gaps 1;

QY 365 CGTGGGTTGAGGACCCGGATCGACGAGCTGCGGGCGACCTAGGGATGTCGA 424
 134 CATGTGAAACACAACTATAGACAGACAGTGCTGGAGGGCAANGCGATTGGCGA 193

QY 425 ACAGAAAAAGCTGCTGACTGCGCATGCGTGGCTTGGAGGCAACGCNATANGTGCCCG 484
 194 ACCGACAAAGCGTGTGGATGCAAAAGGGACCTAGGGATGTCGA 253

QY 485 ACGGGAATTGTTGTTGACAGACTCGGGACNATGGATCCCGTGTGGCGCC 544
 254 ATGGTGTAT-----GTCTACACGGTACACGTTGCGCTTGGGATTTAA 306

QY 545 GGGACACTANATAACCCGTCNCTCAANGAAGTGTGCCCTCTGGATCCCTTAAC 604
 307 AAAGAAGGACACTCCGGTTGCGCTGCCAACAGGCCCTGGGATTTAA 366

QY 605 NCNAANTGAAATCTCNCNCNANGAAGAAGACTCNNTATGACAGCTTANANATCCAT 664
 254 ATGGTGTAT-----GTCTACACGGTACACGTTGCGCTTGGGATTTAA 306

Db 665 GGACNCNGTGTCCCTGTCACATGCCAATGGGG 698
 427 GGCGGAGGGTGAAGTTACATCGTTAACGCCG 460

RESULT 14
 US-08-232-463-14
 Sequence 14, Application US/08232463
 ; Patent No. 5670367
 ; GENERAL INFORMATION:
 ; APPLICANT: DORNER, F.
 ; APPLICANT: SCHEFFLINGER, F.
 ; APPLICANT: FALKNER, F.G.
 ; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 1800 Diagonal Road, Suite 500
 ; CITY: Alexandria
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22313-0299
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/232,463
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/935,313
 ; FILING DATE:

APPLICATION NUMBER: EP 91 114 300.6
 FILING DATE: 26-AUG-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.
 REGISTRATION NUMBER: 29,768
 REFERENCE/DOCKET NUMBER: 30472/114 TMMU
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703)836-9300
 TELEFAX: (703)683-4109
 TELEX: 899149
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7218 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 CLONE: PTZPPT-F1S
 US-08-232-463-14

Query Match 5.7%; Score 46; DB 1; Length 7218;
 Best Local Similarity 3.9%; Pred. No. 0.0005; Mismatches 147; Indels 0; Gaps 0;
 Matches 13; Conservative 175; Mismatches 147; Indels 0; Gaps 0;

Qy 464 GCAACCGNATANGTGGCCGGACGGGAAATTGTTGTTGAGACACTCGGGGACNAT 523
 Db 1037 GCTTGGTGTGAGTCAGGTGGAGCTTGCGATYYYYYYYYYYYYYYYYYYYYYYYY 1096
 Qy 524 GATCCCGGTGATCCCTGCCGGAAACATPANATACCCGTCNTCCAANGAATGCCC 583
 Db 1097 YY 1156
 Qy 584 CCTCTGGGATGCCCTTAACNCNAATGGAATCTCNCTNANGAAGAACTCNNTATG 643
 Db 1157 YY 1216
 Qy 644 AACAGTTAANACNATGATGACNNGTCTCGTCCACATGCCAATGGCGCTGC 703
 Db 1217 YY 1276
 Qy 704 NTACACCANCCATTGTTCTCCCAACNCTCTCTCCNNGCCTCNCCTCCAAATGCAAC 763
 Db 1277 YY 1336
 Qy 764 CNCCGGGAATTCTCTGTCCTCCCTCTCCCTCTCTCT 798
 Db 1337 YY 1371

RESULT 15
 US-08-290-448A-75
 ; Sequence 75, Application US/08290448A
 ; Patient No. 5676954
 ; GENERAL INFORMATION:
 ; APPLICANT: Rogers, Bruce
 ; APPLICANT: Klapper, David G.
 ; APPLICANT: Ratnar, Thorunn
 ; APPLICANT: Kuo, Mel-chang
 ; TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
 ; NUMBER OF SEQUENCES: 93
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LARIVE & COCKFIELD
 ; STREET: 60 State Street, suite 510
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109-1875
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:

Search completed: June 19, 2003, 13:35:16
 Job time: 56 secs

APPLICATION NUMBER: US/08/290,448A
 FILING DATE: August 15, 1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/529, 951
 FILING DATE: May 29, 1990
 APPLICATION NUMBER: US 07/325, 365
 FILING DATE: March 17, 1989
 ATTORNEY/AGENT INFORMATION:
 NAME: ANY E. Mandragoras
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: IM1-018CN
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-77400
 TELEFAX: (617)594-1770
 INFORMATION FOR SEQ ID NO: 75:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1320 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE: NAME/KEY: CDS
 LOCATION: 1..1320
 US-08-290-448A-75

Query Match 5.4%; Score 43.8; DB 1; Length 1320;
 Best Local Similarity 51.8%; Pred. No. 0.0011; Mismatches 0; Mismatches 154; Indels 7; Gaps 4;
 Matches 173; Conservative 175; Mismatches 0; Mismatches 154; Indels 7; Gaps 4;

Qy 365 CCTGGGTTACGGCACCCGATCGACCACTGCTGCGGTGCGACCCGTATGGCCATGTC 424
 Db 131 CATGTGAGCACTCAGATTAGAACAGAAGTGGGAGGGAAAGCGGATTTGGAGRA 190
 Qy 425 ACAGAAAAGCTCGTGAATGGCGATGGCTTGTGACGCAACGCAATANGTGGCG 484
 Db 191 ACCGACAGCGTGTAGCCAAAGGAAAC-TACGGCGRAA 249
 Qy 485 ACGGGGATTTGTTGTTGTTGAGCAAGTCCGGGAATGATCCCGTGAAATCTCGGCC 544
 Db 250 TGGGGATGTCACAGGTCAACAGCAATCTAGATGATGAT-GTTCACAAATCCAAAGA 308
 Qy 545 GGGACACTTANATACCCGTONTCCHANGAATGTSCCCCCTCTGGATCCCTTAAC 604
 Db 309 AGGCACACTCCGTTGCTGCGCCAAACAG---GCCCTGGGATCATTTAAA 364
 Qy 605 NONAATGGAATCTCNCCTNANGAAGAACCTCTATGAAAGCTCTNATGAAAGCTTAACNATGAT 664
 Db 365 ATGATATGGTGT-TAATTGAAATCAGAGCTGTCGTTAACAGCGCACGACATCGAT 423
 Qy 665 GGCACNCNGTGTCTCGTGCACATGGCAATGCG 698
 Db 424 GGCGAGGGGTGAAGTGTAAATCATTACGGAG 457



GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

ON nucleic - nucleic search, using sw model
Run on: June 19, 2003, 12:40:30 ; Search time 123 Seconds
(without alignments)

9615.824 Million cell updates/sec
Title: US-09-966-881-13
Perfect score: 806

Sequence: 1 TGTCTCTCTCGATCACA.....TCCCCCTCTCTAGGATNG 806

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 2085038

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

1: /cgn2_6/_ptodata/1/_pubpna/_us07_pubcomb.seq:/*
2: /cgn2_6/_ptodata/1/_pubpna/_ptct_new_pub.seq:/*
3: /cgn2_6/_ptodata/1/_pubpna/_us06_new_pub.seq:/*
4: /cgn2_6/_ptodata/1/_pubpna/_us05_pubcomb.seq:/*
5: /cgn2_6/_ptodata/1/_pubpna/_us07_new_pub.seq:/*
6: /cgn2_6/_ptodata/1/_pubpna/_ptctus_pubcomb.seq:/*
7: /cgn2_6/_ptodata/1/_pubpna/_us08_pubcomb.seq:/*
8: /cgn2_6/_ptodata/1/_pubpna/_us08_pubcomb.seq:/*
9: /cgn2_6/_ptodata/1/_pubpna/_us09_new_pub.seq:/*
10: /cgn2_6/_ptodata/1/_pubpna/_us09_pubcomb.seq:/*
11: /cgn2_6/_ptodata/1/_pubpna/_us10_new_pub.seq:/*
12: /cgn2_6/_ptodata/1/_pubpna/_us10_pubcomb.seq:/*
13: /cgn2_6/_ptodata/1/_pubpna/_us60_new_pub.seq:/*
14: /cgn2_6/_ptodata/1/_pubpna/_us60_pubcomb.seq:/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	778	96.5	806	10 US-09-966-881-13
2	543.8	67.5	727	10 US-09-966-881-16
3	533.6	67.5	724	10 US-09-966-881-18
4	142.8	17.7	842	10 US-09-966-881-17
5	134.6	16.7	687	10 US-09-966-881-14
6	124.2	15.4	1116	9 US-09-938-842A-1004
7	110.4	13.7	1215	9 US-09-938-842A-58
8	93.4	11.6	460	10 US-09-770-444-439
9	93	11.5	479	10 US-09-924-174
10	74.4	9.2	1629	9 US-09-938-842A-1766
11	68.4	8.5	277	10 US-09-923-876-484
12	64.4	8.0	1185	9 US-09-938-842A-809
13	56.2	7.0	388	10 US-09-878-574-363
14	54	7.0	741	10 US-09-966-881-15
15	41	5.1	1137	10 US-09-828-205-3
C	16	37.6	4.7	481 9 US-09-918-905-25
C	17	37.4	4.6	708 9 US-10-123-298
18	35.6	4.4	360	10 US-09-864-761-2734
19	4.4	4.4	496	10 US-09-864-761-10689

ALIGNMENTS

RESULT 1
US-09-966-881-13
Sequence 13, Application US/09966881
; Patent No. US20020120960A1
; GENERAL INFORMATION:
; APPLICANT: Seymour, Graham
; Bird, Colin
; Medina-Suarez, Rosybel
TITLE OF INVENTION: Genetic control of Fruit Ripening
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
; ADDRESSE: Zeneca Ag Products Inc.
; STREET: 1800 Concord Pike
; CITY: Wilmington
; STATE: DE
; COUNTRY: USA
; ZIP: 19850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOSS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/966,881
; FILING DATE: 28-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/09/242,860
; FILING DATE: 29-Mar-1999
; APPLICATION NUMBER: GB 9618862.8
; FILING DATE: 10-Sep-1996
; APPLICATION NUMBER: GB 9703366.1
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: PCT/GB97/02424
; FILING DATE: 08-Sep-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenkutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: SEE 50183/UST
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 886-1699
; INFORMATION FOR SEQ ID NO: 13:

GENERAL INFORMATION:

APPLICANT: Seymour, Graham

Bird, Colin

Medina-Suarez, Rosybel

TITLE OF INVENTION: Genetic control of Fruit Ripening

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESSEE: Zeneca Ag Products Inc.

STREET: 1800 Concord Pike

CITY: Wilmington

STATE: DE

COUNTRY: USA

ZIP: 19850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/242, 860

FILING DATE: 28-Sep-2001

CLASSIFICATION: <Unknown>

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US/09/242, 860

FILING DATE: 29-Mar-1999

APPLICATION NUMBER: GB 9618862.8

FILING DATE: 10-Sep-1996

APPLICATION NUMBER: GB 9708366.1

FILING DATE: 25-APR-1997

APPLICATION NUMBER: PCV/GB97/02424

FILING DATE: 08-SEP-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hohenschutz, Liza D.

REGISTRATION NUMBER: 33, 712

REFERENCE/DOCKET NUMBER: SEE 50183/UST

TELECOMMUNICATION INFORMATION:

TELEPHONE: (302) 886-1699

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 842 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: cDNA

IMMEDIATE SOURCE:

CLONE: U-0115

SEQUENCE DESCRIPTION: SEQ ID NO: 17:

US-09-966-881-17

Query Match 17.7%; Score 142.8; DB 10; length 842;

Best Local Similarity 64.3%; Pred. No. 1.9e-36; 0; Mismatches 276; Conservative 0; Indels 9; Gaps 5;

Matches 276; Conservative 0; Mismatches 144; Indels 9; Gaps 5;

Qy 325 ATATCACAGCAGCGCTCGCAGATCTCTGGTATCTCGCGGGTCAGGCCAACCG 384

Db 140 AGAGAGCTGAGACGCTGCGGCGCGACTGTTGGCTACTTGTCACTGGGCACTGG 199

Qy 385 ATGGACGACTGCTGGCGGGCGGCGACCTCTATGGCATGTCACAGAAAGCTGCTGAC 444

Db 200 ATGGACGACTGCTGGCGGGCTGACGGCTGACACGGCGAGGGCTGCTGAC 259

Qy 445 TSGGGCATGGCTTGGACGCAACGCAATGCTGGGAAATTGGTGTGTTG 504

Db 260 TGGCCCATGGGTTGGGAGAACGGGAG-AGATATAGCTGGT 318

Qy 505 GAGAGACTCCGGGACAGTATGCTGGGAACTATACCCG 564

Db 319 GACCGACAGTGGGACAGNAGA-CCCGCGAACGGGACGGTCCGTTACCGCG 377

Qy 565 TGNCCAANGAAGTGTGCCCTCTGGGAAACCCCTTAACACNCNAAATGGAAATCTCNCTC 624

Db 378 TCACTC--AGGAGGCCGCTGGTGTATCTCAAGCGGCCAGATGGTCATCCAGT- 432

US-09-966-881-14

Query Match 16.7%; Score 134.6; DB 10; Length 687;

Best Local Similarity 61.6%; Pred. No. 8.5e-34; 0; Mismatches 163; Indels 9; Gaps 5;

Matches 276; Conservative 0; Mismatches 163; Indels 9; Gaps 5;

Qy 325 ATATCACAGCAGCGCTCGCAGATCTCTGGTATCTGGTCTGGCGGCTGAGCAACCG 384

Db 140 AGAGAGCTGAGACGCTGCGGCGCGACTGTTGGCTACTTGTCACTGGGCACTGG 199

Qy 625 NANGGAGAACTCTWATGACAGCTTANACNATGATGGACAGCNCNGCTCTCGTCCA 684

Db 433 GAAGGAGGCTCATGACTGACATCGACAGCCATGACGCGGGCGCCAGGTC 492

Db 685 CATGCCAATGGCGCTGENTCACCCAGAACATTCTCCCAAGNTCTCTCCNTNGCC 744

Db 493 CATGCCAATGGCGCTGENTCACCCAGAACATTCTCCCAAGNTCTCTCCNTNGCC 550

Qy 745 TCCNCTCCC 753

Db 551 TCCACATCC 559

QY 385 ATCGACGACTGCTGGCGCTGGCACCTGATGGCATGTCACAGAAAAGCTCGTGCAC 444
 Db 200 ATCGACGACTGCTGGCGCTGGCACCTGATGGCATGTCACAGAAAAGCTCGTGCAC 259
 QY 445 TCGGGATTGGCTTGGACGCAACGCAATANGTGCCCGACGGGAATTGGTGTGTTG 504
 Db 260 TCGGCCATCGGGTCTGGAAAGAACGGATGGGACGGGAGATGGTGTGTTG 318
 QY 505 GACAGACTCCGGAAATGATGCCGAACTTCAGGGACGGGAGATGGTGTGTTG 564
 Db 319 GACCGAGACTGCGACACNA-CCCGTCACCGAACGGGACGGGAGATGGTGTGTTG 377
 QY 565 TCTCCRANGAAGT3CCCCCTGGAATCTCTCCACANAGACCATGACGCCGGCGCAGC 624
 Db 378 TCATCCANGAAGGAGCGCCTGT--GGATCATCTTCAGGGACATGGTCATCCAGTC 434
 QY 625 NANGGAGAACCTNTATGAA-CAGCTTAANACNATCGATGACAGCNGTGTCTC 682
 Db 435 AAGGAAGGAGCCTCATGATGAACTCCACANAGACCATGACGCCGGCGCAGC 494
 Db 683 CACATGCCAATGGCCCTGCTCACCCANCCATTNTCCCAACNCTCTTCNCNTG 742
 Db 495 CACATTCGGGGGGCGTGCACACACC--AGTNGTCNCAACATCATCTCAGGG 552
 QY 743 CCTCCNOTCCCAATGCAACCCNCCGG 770
 Db 553 GCGTCCACTTCCACNATGCAANACAGGG 580
 RESULT 6
 US-09-938-842A-1004
 ; Sequence 1004, Application US/09938842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; FILE REFERENCE: SCRIP1300-3
 ; CURRENT FILING NUMBER: US/09/938 842A
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227, 866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264, 647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300, 111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO: 58
 ; LENGTH: 1215
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 ; US-09-938-842A-58
 Query Match 15.4%; Score 124.2; DB 9; Length 1116;
 Best Local Similarity 60.2%; Pred. No. 9.1e-26;
 Matches 241; Conservative 0; Mismatches 152; Indels 7; Gaps 3;
 QY 319 ATGACCAATACTAACAGCACCGCTCCAGATCTCTGGTTACTCTGCTGGCTTCAGC 378
 Db 1 ATGAGGTGTGAGAAACCATACCGAGAGGAAACTAGGTGTTACHTGCGGAAACAGGA 60
 QY 379 AACCCATCGACGACTCTGGGGTGGACCCCTGATGGCATGTCACAGAAAAGCTC 438
 Db 61 AACCCATCGACGATGGCTGGCATGACCCCAATGACAAACGGATTAACCGCTA 120
 QY 439 GCTGACTGCGGATTGGCTTGGACGAAACGGAATANGTGCCGACGGGAATTGGT 498
 Db 121 GGGGATGCGGATGCGATTGGAAAGAACGGATCGGTGGTGTGATGGACGA-TCCTA 179
 QY 499 CGTGTGACGACTCGGGGACNATGATCCCGTGAATCCCTCCCGGACACTTANAT 558
 Db 180 CTAGTCACCTACCCAGAGACAT-CGGTTACCTCAGACCGGGGTTACGGTC 238
 QY 559 AACCCCTCNTOCAANGAAGTGTGCCCCTCTGGATOCCTTAAACCNCAANTGAAAC 618
 Db 239 AGCCCTGTGATCAG---ACCGACACTATGGATCGTTCAACGTGACATGGTAT 293
 QY 619 TCTCTCANGAAGAACCTNTATGACACGACTTAAACNATCGATGACACNCTGTCT 678
 Db 294 TCACTTAAACAAAGACCTATAGTTACAGTTCACAGTCAACAGTCATGGACCTGGGC 353
 QY 679 CGTCCACATGCCAATGGCCCTGCTGCCACCCANCCATT 718
 Db 354 CGTCACATCTAACGGTGTGCACTCACATTCACTAGTT 393
 RESULT 7
 US-09-938-842A-58
 ; Sequence 58, Application US/09938842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; FILE REFERENCE: SCRIP1300-3
 ; CURRENT FILING NUMBER: US/09/938 842A
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227, 866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264, 647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300, 111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO: 58
 ; LENGTH: 1215
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 ; US-09-938-842A-58
 Query Match 13.7%; Score 110.4; DB 9; Length 1215;
 Best Local Similarity 59.0%; Pred. No. 9.1e-26;
 Matches 239; Conservative 0; Mismatches 159; Indels 7; Gaps 4;
 QY 353 TTGGTTATCTGCTGGCGGGTAGGCAACCGATGACGAGCTGCGGGGGGAGCCTG 412
 Db 147 TAGGTACCTACGATGACGCGCAAACTACGACTGAGCTGTTGGTGTGACCTC 206
 QY 413 ATGGCATGCAACAGAAAAGCTGCTGCTGCGCATGGCAATGGCTTGGACGACGCA 472
 Db 207 ACTGGAGCACACCGTCAAGCTCTGGCTGACTGCCATGGATGGCAAAAGGCCA 266
 QY 473 TANGTGCCGGACGGGAATTGGTGTGACGACGACTCGGGACNATGATCCCGT 532
 Db 267 TGGTGGCCGCTGAC-GGTGCGATCTACGTGTCACCGACTGAGAACGA-CAACCGAT 324
 QY 533 GAATCCTCGCCGGGACACTTANATACCCGCTNCTCAANGAAGSTGGCCCTCTGGA 592
 Db 325 TAGGCCAAGCCGGGACTTAAAGACCGGGTGGCT---AGACGAGGACTCTGGA 380
 QY 593 TCCCTTAACNCAANTGGAATCTCNCTCANGAAGACACTCTTAAACAGCTT 652
 Db 381 TCATCTCCACGAGACATGAGATCAGCTCAA-GAAGGACTAATCATGAACTCATC 439
 QY 653 ANACNATCGATGGACNCNGTGTCTCGTCCACATGCCAAAGGCCCTGNTCACANC 712
 Db 440 AGACCATCGTGGCGTGTCTCGTACACATCTCTGGGGCTTACAGATCAGTC 499

RESULT 8
US-09-770-444-439
Sequence 439, Application US/09770444
; Patent No. US20020033280A1
GENERAL INFORMATION:
APPLICANT: Gorlach, Jorn
APPLICANT: An, Long-Qiang
APPLICANT: Hamilton, Carol M.
APPLICANT: Price, Jennifer L.
APPLICANT: Raines, Tracy M.
APPLICANT: Yu, Yang
APPLICANT: Rameaka, Joshua G.
APPLICANT: Page, Amy
APPLICANT: Matthew, Abraham V.
APPLICANT: Ledford, Brooke L.
APPLICANT: Woesner, Jeffrey P.
APPLICANT: Haas, William David
APPLICANT: Garcia, Carlos A.
APPLICANT: Krikke, Maja
APPLICANT: Slader, Ted
APPLICANT: Davis, Keith R.
APPLICANT: Allen, Keith
APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
FEATURE: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
'
CURRENT APPLICATION NUMBER: US/09/924,035A
CURRENT FILING DATE: 2000-08-11
PRIORITY APPLICATION NUMBER: US 60/148,784
PRIORITY FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 900
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO: 174
LENGTH: 479
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(479)
OTHER INFORMATION: n = A,T,C or G
US-09-924-035A-174
Query Match 11.5%; Score 93; DB 10; Length 479;
Best Local Similarity 61.0%; Pred. No. 3.1e-20;
Matches 178; Conservative 0; Mismatches 112; Indels 2; Gaps 2;
CURRENT FILING DATE: 2001-01-26
PRIORITY APPLICATION NUMBER: 60/178,502
PRIORITY FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 439
LENGTH: 460
TYPE: DNA
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(460)
OTHER INFORMATION: n = A,T,C or G
US-09-770-444-439
Query Match 11.6%; Score 93.4; DB 10; Length 460;
Best Local Similarity 59.7%; Pred. No. 2.3e-20;
Matches 182; Conservative 0; Mismatches 121; Indels 2; Gaps 2;
Db 268 GCGAGCAGAGCCGCACTGACGACGCCCGAGGGAGGTGCTTGACGGCTCTGTGATGCCATA 327
Db 146 GCGGNNNGGAATTCGAGATGAGCTGCGACGAATGTCGGCTTGACAGAAATGAGTGTGTC 205
Query 328 ATCACACGACACGGCTCGAGATCTGTGATGAGCTGCTGGCTGAGCTGGCAACCGATC 387
Db 206 AGAACCATACGAGAGGAGAACCTAGGTACTTACTTGTGGCAACGAAACCTATC 265
Query 388 GAGGAGCTGCTGGGGCGACCCCTGATGGCAGTCACAGAAAAAGCTCGGTGACTGCG 447
Db 266 GAGGATGTTGGGATGTGACCCATATGGCACAAAGAACGCTAGGGATTC 325
Query 448 GCGATTCGCTTGACGCAACGCGNATANGTGGCCGGACGGGAATTGTCGTGTCG 507
Db 326 GGTATCGGATTTGGAGAAACCGGATCGGGTGGTGTGACGAA-TTCTACCTGATGCA 384
Query 508 AGACTCCGGGAGATGACCCCGTGAATCTGGCCCGGAAACTTANATACCCGTCN 567
Db 385 TGACCCAGAGACGACAAAT-NNGGTTAACCTTAGCTCACGCCGCTGA 443
568 TCCAA 572
|||||

RESULT 9
US-09-924-035A-174
; Sequence 174, Application US/09924035A
; Patent No. US20020142319A1
GENERAL INFORMATION:
APPLICANT: Gorlach, Jiri
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 201105
CURRENT APPLICATION NUMBER: US/09/924,035A
CURRENT FILING DATE: 2000-08-11
PRIORITY APPLICATION NUMBER: US 60/148,784
PRIORITY FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 900
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO: 174
LENGTH: 479
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(479)
OTHER INFORMATION: n = A,T,C or G
US-09-924-035A-174
Query Match 11.5%; Score 93; DB 10; Length 479;
Best Local Similarity 61.0%; Pred. No. 3.1e-20;
Matches 178; Conservative 0; Mismatches 112; Indels 2; Gaps 2;
CURRENT FILING DATE: 2001-01-26
PRIORITY APPLICATION NUMBER: 60/178,502
PRIORITY FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 439
LENGTH: 460
TYPE: DNA
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(460)
OTHER INFORMATION: n = A,T,C or G
US-09-770-444-439
Query Match 11.6%; Score 93.4; DB 10; Length 460;
Best Local Similarity 59.7%; Pred. No. 2.3e-20;
Matches 182; Conservative 0; Mismatches 121; Indels 2; Gaps 2;
Db 268 GCGAGCAGAGCCGCACTGACGACGCCCGAGGGAGGTGCTTGACGGCTCTGTGATGCCATA 327
Db 146 GCGGNNNGGAATTCGAGATGAGCTGCGACGAATGTCGGCTTGACAGAAATGAGTGTGTC 205
Query 328 ATCACACGACACGGCTCGAGATCTGTGATGAGCTGCTGGCTGAGCTGGCAACCGATC 387
Db 206 AGAACCATACGAGAGGAGAACCTAGGTACTTACTTGTGGCAACGAAACCTATC 265
Query 388 GAGGAGCTGCTGGGGCGACCCCTGATGGCAGTCACAGAAAAAGCTCGGTGACTGCG 447
Db 266 GAGGATGTTGGGATGTGACCCATATGGCACAAAGAACGCTAGGGATTC 325
Query 448 GCGATTCGCTTGACGCAACGCGNATANGTGGCCGGACGGGAATTGTCGTGTCG 507
Db 326 GGTATCGGATTTGGAGAAACCGGATCGGGTGGTGTGACGAA-TTCTACCTGATGCA 384
Query 508 AGACTCCGGGAGATGACCCCGTGAATCTGGCCCGGAAACTTANATACCCGTCN 567
Db 385 TGACCCAGAGACGACAAAT-NNGGTTAACCTTAGCTCACGCCGCTGA 443
568 TCCAA 572
|||||

RESULT 10
US-09-938-842A-176
Sequence 176, Application US/09938842A
; Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
FEATURE: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIORITY APPLICATION NUMBER: US 60/227,866
PRIORITY FILING DATE: 2000-08-24
PRIORITY APPLICATION NUMBER: US 60/264,647
PRIORITY FILING DATE: 2001-01-16
PRIORITY APPLICATION NUMBER: US 60/3300,111
PRIORITY FILING DATE: 2001-06-22

RESULT 13

US 09-878-574-3663

Sequence 3663, Application US/09878574

Patent No. US2002011548A1

GENERAL INFORMATION:

APPLICANT: Byrum, Joseph R.

APPLICANT: La Rosa, Thomas J.

APPLICANT: Thompson, Michael D.

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(15401)B

CURRENT APPLICATION NUMBER: US/09/878, 574

CURRENT FILING DATE: 2001-12-21

PRIORITY NUMBER: 09/33, 535

PRIORITY FILING DATE: 1999-06-14

NUMBER OF SEQ ID NOS: 15775

SEQ ID NO 3663

LENGTH: 388

TYPE: DNA

ORGANISM: Glycine max

OTHER INFORMATION: Clone ID: LIB3028-007-Q1-B1-E8

US-09-878-574-3663

Query Matchⁿ 7.0%; Score 56 2; DB 10; Length 388; Best Local Similarity 52.5%; Pred. No. 3.2e-08; Matches 189; Conservative 0; Mismatches 164; Indels 7; Gaps 4;

Qy 378 CAACCCGACGAGACTGCTGGGGTGCACCCGATGCGATGCAACAGAAAAGCT 437

Db * 35 CAACCCGATGACGCTTGAGATGCAATAAGACTGCGCCATGACGGGTTAGCT 94

Qy 438 CGCTGACTCGGGCATGGGTTGGACGCAACGCAATANGTGGCGCGACGGGATTTG 497

Db 95 AGCCAACTGCGCAAAAGGGTTCGGAAGGGGCCGGCTGGTCCATCA 154

Qy 498 TCGTGTGAGACTCGGGGACAGATGGAGATGACGCCCTGAACTCTGGGGAGACACTTAA 557

Db 155 T-GRGTCACCGATAATTCCGATGACGA-CATGGTAACCTAAGCCGGAACTATCGT 212

Qy 558 TACCCGGRNTCCANGAAGTGTGCCCCCTCTGGATCCCTTAACACNAANGAAT 617

Db 213 CACGCTGTACCCAAAAGG---CCCTTGTGATCATCTTCGGACACAGATGATC 268

Qy 618 CTCTCTCNGANGAAGACTNTTGTACAGCTTAACACATGATGGACNCNGTGTCC 677

Db 269 CAGTT-GAGCAAGAGCTGATGATTCTCCGACAGAACATGATGTCGGCGCAA 327

Qy 678 TCGTGTGACATGGCAATGGCGGCCCTGCTACACCAACATTTCNTCCCAACNCTCTC 737

Db 328 ACGTGCAATTAGGGCGCTGCTGCCCTACCCATTCACTGTCGACACAGTTATTATCC 387

RESULT 14

US 09-966-881-15

Sequence 15, Application US/09966881

Patent No. US20020120960A1

GENERAL INFORMATION:

APPLICANT: Seymour, Graham

Bild, Colin Medina-Suarez, Rosybel TITLE OF INVENTION: Genetic control of Fruit Ripening

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESSEE: Zeneca Ag Products Inc. STREET: 1800 Concord Pike CITY: Wilmington STATE: DE COUNTRY: USA ZIP: 19850

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/966, 881

FILING DATE: 28-Sep-2001

CLASSIFICATION: <Unknown>

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US/09/242, 860

FILING DATE: 29-Mar-1999

APPLICATION NUMBER: GB 9618862.8

FILING DATE: 10-SEP-1996

APPLICATION NUMBER: GB 9708366.1

FILING DATE: 25-APR-1997

APPLICATION NUMBER: PCT/CB97/02424

FILING DATE: 08-SEP-1997

ATTORNEY/AGENT INFORMATION:

NAME: Wohenshutz, Liza D.

REGISTRATION NUMBER: 33-712

REFERENCE/DOCKET NUMBER: SEE 50183/US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (302) 886-1699

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

IMMEDIATE SOURCE:

CLONE: U-084

SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-09-966-881-15

Query Match 5.4%; Score 43 6; DB 10; Length 741; Best Local Similarity 65.6%; Pred. No. 0.00056; Matches 84; Conservative 0; Mismatches 41; Indels 3; Gaps 2;

Db 1 TCCACATGCGCAATGCGCTGCAATCNC-AGTACATCACCACTCATCCAT 59

Qy 681 TCCACATGCGCAATGCGCTGCGNCACNCCAAATTCNTCCCAACNCTCTCTCCNT 740

Db 741 NGCCCTCCNCNTCCC---AATGCAACCCNCGGGAATTCCTNGTCCCCNCCTCCCTCTCC 798

Db 60 GGCCGCCACATCCACAGACTGCAAGCCACGGGGATGCCCTGGCCAGCTCTCTCT 119

Qy 799 ATGGTNG 806

Db 120 CACTATGG 127

RESULT 15

US-09-820-505-3

Sequence 3, Application US/09828505

Patent No. US20020142978A1

GENERAL INFORMATION:

APPLICANT: Raz, Eyal

APPLICANT: Takabayashi, Kenji

APPLICANT: Nguyen, Minh-Duc

TITLE OF INVENTION: Synergistic Improvements to

TITLE OF INVENTION: Polynucleotide Vaccines

FILE REFERENCE: 6510-203

CURRENT APPLICATION NUMBER: US/09/828, 505

CURRENT FILING DATE: 2001-04-06

PRIORITY NUMBER: 60/195, 890

PRIORITY FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 1137

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: hsshadelta36Ambar nucleic acid sequence

US-09-828-505-3

Query	Match	5.1%	Score	41	DB	10	Length	1137
Best	Local	Similarity	56.5%	0	Pred.	No.	0.0048	
Matches	74	Conservative	0	P mismatches	57	Indels	0	Gaps
QY	365	CGTGGGGTTCAGCCACCCGATCGACGTGCGTGGTGCACCTGTATTGGCATGTCA						
	1							
Db	74	CCTCCGGAGCTTACACATTATTGATGGCTGTGGAGGGGAAGGCAGATTGGCCGAA						
QY	425	ACGAAAAAAGCTCGTCACTGGGCACTGGCATTTGGACGCAACGCAATANGTGGCGG						
	1							
Db	134	ACCGCAAGGCACTGGCTGACTGTGCCCAAGGTTGGCAAAGGTACCGTGGTGCAGG						
QY	485	ACGGGGAATT 495						
	1							
Db	194	AGGGAGACATT 204						

Search completed: June 19, 2003, 13:34:04
Job time : 124 secs

THIS PAGE BLANK (USPTO)